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(57) Abstract

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

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T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF USING SAME

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TECHNICAL FIELD OF THE INVENTION

The present invention relates to cloned T-type calcium channels.

BACKGROUND OF THE INVENTION

Biological membranes are themselves generally impermeable to ionic species. Thus, ions enter cells through regulated pores formed from membrane-associated proteins. Most of these regulated pores are voltage-dependent and are thus able to transduce changes in the transmembrane potential into ion flux. Voltage-gated ion channels form a "superfamily" of related proteins (cf. Jan et al., *Nature*, *345*, 672 (1990)). Peculiar to this genus is a high degree of conservation in molecular structure. Generally, voltage-gated channels are membrane bound glycolsylated proteins formed of many subunits. Large α subunits form a pore in the membrane that is selective for a given ionic species. Each α subunit contains four domains (I, II, III, and IV). Each channel domain has six putative transmembrane helical segments (S_1-S_6). In general, the segments within each domain are similar but not identical. Aside from overall structural conservation, certain charged residues within the domains are highly conserved among voltage-gated ion channels (Jan et al., *supra*; Stühmer et al., *Nature*, *339*, 597-603 (1989)).

Differences in charged residues between groups of voltage-gated ion channels confer properties unique to each subgroup, such as ion selectivity. For example, most voltage gated ion channels are selective for either sodium, potassium or calcium. Known calcium channels require a ring of negative charge provided by glutamate residues found at similar locations in each of the domains (Yang et al., *Nature*, *366*, 158-61 (1993)).

Voltage-gated channels are often classified on the basis of their electrophysiology. The resting membrane potential of most animal cells is between about −70 mV and −80 mV. When the membrane becomes depolarized (moved towards 0 mV), various membrane channels become activated (they are said to

"open"). Thus, one basis for classifying membrane channels is the membrane potential necessary to activate (or "gate") them (voltage dependency). For example, "T-type" calcium channels are activated at a lower voltage than L- or N-type channels (Nowycky et al., *Nature, 316*, 440-43 (1985)). Other physiological properties are the activation kinetics, inactivation kinetics, tail current (deactivation kinetics), and single channel conductance. Thus, in comparison to other calcium currents, T-type calcium current is characteristically short (Chen et al., *J. Gen. Physiol., 96*, 603-30 (1990)), and it exhibits characteristically slow activation kinetics near threshold, fast inactivation kinetics, and slow tail current (Randall et al., *Neuropharmacol., 63*, 879-93 (1997); Carbone et al., *Nature, 310*, 501-02 (1984); Nilius et al., *Nature, 316*, 443-46 (1985)).

Calcium currents have been implicated in many neurological and muscular functions. For example, T-type calcium current is associated with cardiac pacemaker activity, pain transmission in the central nervous system, and in other physiological functions. Defects in T-type calcium current have been implicated in cardiac arrhythmia, hypertension, and epilepsy. Given their potential clinical value, the pharmacological properties of calcium channels have been the subject of extensive study. Most such studies have involved L-type channels because, unlike T-type channels, L-type calcium channels are readily purified from cell extracts. For example, L-type calcium channels have been purified using dihydropyridine drugs (e.g., nifedipine) which can bind with sufficiently high affinity to serve as a ligand for purifying L-type calcium channels. Such purified and cloned L-type calcium channels have been used to develop assays for drugs affecting L-type calcium channels (see, e.g., U.S. Patents 5,429,921 and 5,386,025).

While many electrophysiological characteristics of T-type calcium currents are known, the lack of isolated T-type channels has stalled research into the pharmacology and biophysics underlying the T-type calcium current, at least in comparison with other calcium channels. Indeed, while it is generally assumed that voltage-sensitive ion channels are responsible for the current, no such channel protein, nor any nucleic acid encoding such a protein, has been isolated. In view of the foregoing problems, there exists a need for an isolated T-type calcium channel and a nucleic acid encoding a T-type calcium channel.

BRIEF SUMMARY OF THE INVENTION

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or

substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

The present invention is useful for exploring the electrophysiology and pharmacology of the T-type calcium current. Such knowledge can lead to the development of drugs for potentiating or attenuating T-type calcium channels. Thus, the present invention provides an assay for identifying potential drugs affecting T-type calcium channels by exposing cells expressing a T-type calcium channel to a putative drug and then measuring the calcium flux in response to a change in membrane potential. The identification of drugs affecting T-type calcium channels will facilitate even greater understanding of the biophysics of these proteins. Furthermore, some such drugs could have potential clinical applications.

The invention can best be understood with reference to the accompanying drawings and in the following detailed description of the preferred embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E compare the complete amino acid sequences of three types of T-type calcium channels (α1G (or Ca_vT.1), α1H (or Ca_vT.2), and α1I (or Ca_vT.3)), indicating conserved functional domains.

Figures 2A-2D are graphic representations of the current-voltage relationships of three cloned T-type calcium channels (Figures 2A, 2B, and 2C) and a cloned R-type calcium channel (Figure 2D).

Figure 3A is a graphic representation of the average current-voltage curve for cloned T-type calcium channels (α1G, triangles, α1H, inverted triangles, α1I, circles), and a cloned R-type calcium channel (filled squares). Figure 3B compares the normalized conductance of a cloned T-type calcium channel at three different concentrations of $BaCl_2$.

Figure 4 depicts average kinetics of the tail current as a function of repolarization potential for α1G (triangles), α1H (inverted triangles), α1I (circles), and a cloned R-type calcium channel (filled squares).

Figures 5A and 5B graphically present data concerning the use of a cloned T-type calcium channel to detect drugs affecting the channel. Figure 6A depicts the effect of 100 μM on current-voltage relationships with a single dosage of mibefradil. Figure 6B illustrates the effect on T-type channel conductance of various doses of mibefradil.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α

subunit. The nucleic acid can be of any type, and it can include other elements aside from a sequence encoding a T-type calcium channel domain or domains. For example, where the nucleic acid comprises RNA, it can also include regulatory sequences suitable to permit translation of the RNA. Thus, an RNA nucleic acid of the present invention preferably has at least one ribosome entry site, and preferably has a polyadenosine tail for stabilizing the RNA in the cellular environment. Similarly, DNA nucleic acids of the present invention can have regulatory elements for promoting the transcription of sequence encoding the T-type calcium channel into an RNA such as that described above. For example, a DNA nucleic acid of the present invention can have a promoter and/or an enhancer sequence. While the nucleic acid can be any type of nucleic acid, the nucleic acid preferably comprises a cDNA. A cDNA nucleic acid is preferred over other nucleic acids to permit the nucleic acid to be readily cloned, sequenced, and expressed in a wide variety of cells.

The choice of promoter and/or an enhancer will largely depend on the milieu in which the nucleic acid is to be expressed. Thus, for expression in bacterial cells, the regulatory elements are bacterial promoters. Similarly, for expression in mammalian cells, the regulatory elements are able to effect expression in mammalian cells. While many such regulatory elements are known in the art, examples include prokaryotic promoters and viral promoters (e.g., retroviral ITRs, LTRs, immediate early viral promoters (IEp), such as herpesvirus IEp (e.g., ICP4-IEp and ICP0-IEp), cytomegalovirus (CMV) IEp, and other viral promoters, such as Rous Sarcoma Virus (RSV) promoters, and Murine Leukemia Virus (MLV) promoters). Other suitable promoters are eukaryotic promoters, such as enhancers (e.g., the rabbit β-globin regulatory elements), constitutively active promoters (e.g., the β-actin promoter, etc.), signal specific promoters (e.g., inducible promoters such as a promoter responsive to RU486, etc.), and tissue-specific promoters (e.g., those active in epidermal tissue, dermal tissue, tissue of the digestive organs (e.g., cells of the esophagus, stomach, intestines, colon, etc., or their related glands), smooth muscles, such as vascular smooth muscles, cardiac muscles, skeletal muscles, lung tissue, hepatocytes, lymphocytes, endothelial cells, sclerocytes, kidney cells, glandular cells (e.g., those in the thymus, ovaries, testicles, pancreas, adrenals, pituitary, etc.), tumor cells, cells in connective tissue, cells in the central nervous system (e.g., neurons, neuralgia, etc.), cells in the peripheral nervous system, and other cells of interest).

The isolated or substantially purified nucleic acid of the present invention encodes all or part of a T-type calcium channel α subunit. As used herein, a "calcium channel" includes a protein structure for facilitating the flux of calcium ions across a biological membrane into which the calcium channel is inserted. As used herein, a "T-type channel" is a type of voltage-gated ion channel that facilitates the flux of ions

when the membrane potential of a biological membrane into which it is inserted experiences a slight depolarization. Thus, a T-type calcium channel can begin to gate from about -60 mV to about -30 mV (i.e., about -45 mV to about -35 mV) in about 10 mM Ba^{2+}. Additionally, T-type channels of the present invention exhibit a slow deactivation (tail current) following depolarization. Thus, a T-type calcium channel can exhibit a tail current that decays exponentially with a tau value from about 1 ms to about 10 ms (e.g., from about 4 ms to about 7 ms, such as about 6 ms) following repolarization to a membrane potential from about -80 mV to about -60 mV in a solution with a Ba^{2+} concentration of from about 10 mM to about 40 mM. Another defining characteristic of T-type calcium channels is that they exhibit small single channel conductance. Thus, for example, a T-type channel exhibits a single channel conductance of from about 4 pS to about 12 pS (e.g., from about 6 pS to about 10 pS), and typically from about 7 pS to about 9 pS in a solution with a Ba^{2+} concentration of about 0.1 M.

The isolated or substantially purified nucleic acid of the present invention encodes all or part of any T-type calcium channel having at least one of the aforementioned electrophysiological properties when properly assembled within a cellular membrane. The general structure of calcium channels is summarized above and is otherwise known in the art. Thus, for example, the nucleic acid can encode one of the four functional domains mentioned above. As used herein, a domain of a T-type calcium channel is any protein structure able to associate with three other domains to form a tetrameric body functioning as a T-type calcium channel. While the native T-type calcium channel structure includes all four domains in a single polypeptide (indicated in Figures 1A-1E), a domain can exist as a polypeptide species separate from those containing the other domains. Such separate domains are able to associate within the plasma membrane to form a functional channel. Alternatively, where a plurality of domains are linked within a common polypeptide, the linkage can deviate substantially from the native linkage. Thus, for example, the domains can be linked by polypeptide sequences other than those sequences linking the domains in the native protein (e.g., non-native polyglutamate linkages). Indeed, the domains themselves can include non-native linkages between membrane-spanning elements within the domains. Aside from these modifications, the nucleic acid can encode a chimeric calcium channel domain (or an entire channel) comprising a portion of a T-type calcium channel and a portion derived from another calcium channel (or other channel) protein. For example, the chimera can include portions of domains from T-type channels responsible for low voltage gating and portions of domains from other calcium channels responsible for slow inactivation. Such a protein exhibiting T-type gating but longer inactivation kinetics would facilitate pharmacological research.

As mentioned, nucleic acids of the present invention can encode an entire T-type channel (i.e., a T-type channel protein comprising four functional domains). It has been discovered that at least three genes encoding T-type calcium channels exist in humans and rats (i.e., α1G (or Ca_v3.1), α1H (or Ca_v3.2), and α1I (or Ca_v3.3)), and alternate splicing of these isoforms exist. Examples of the amino acid sequences of full-length T-type channels, and the sequences of suitable coding nucleic acids are set forth at SEQ ID NOs:1-8 (α1G sequences), SEQ IS NOs:9-10 (α1H sequences), and SEQ ID NOs: 11-12 (α1I sequences). However, the invention is not limited to these exemplary sequences. Indeed, as mentioned, an amino acid sequence of a T-type calcium channel can vary from those listed, and it is within the state of the art to change a nucleotide sequence encoding a T-type channel to introduce mutations into the protein. Indeed, for conducting electrophysiological assays, it may be desirable to introduce mutations into such a protein. For example, mutations comprising insertions or deletions can be introduced on either the amino- or carboxy-terminus of the protein, or such mutations can be intrasequence insertions or deletions. Where the electrophysiological properties of the calcium channel are to be conserved, such mutations preferably are in regions other than the membrane spanning domains. However, in some applications (e.g., to decrease inactivation kinetics), the changes can be within the membrane-spanning regions. Moreover, as mentioned above, the sequence can form a protein having only one functional domain of a T-type calcium channel. Additionally, the sequence can also form a chimeric protein or domain, such as those described above.

Aside from insertions and deletion mutations of native T-type calcium channel sequences, a T-type calcium channel can include substitutions of amino acid residues, e.g., for those indicated in SEQ ID NOs:1-12. Preferably, and especially where such a substitution is within a membrane spanning region, the substitution is conservative. Thus, within membrane spanning domains, positively-charged residues (H, K, and R) preferably are only substituted with positively-charged residues; negatively-charged residues (D and E) preferably are only substituted with negatively-charged residues; neutral polar residues (C, G, N, Q, S, T, and Y) preferably are only substituted with neutral polar residues; and neutral non-polar residues (A, F, I, L, M, P, V, and W) preferably are only substituted with neutral non-polar residues. Preferably, any amino-acid substitution within the membrane-spanning regions does not alter this conservation. Most preferably, any substitution, deletion, or insertion does not alter the IVS4 domain. In each of the exemplary T-type calcium channel α subunit sequences, the putative IVS4 region comprises SEQ ID NO:13. Given the strong sequence conservation among families of voltage-gated ion channels, it is likely that this sequence or a derivative sequence, will be present in T-type channels. Thus, the

present invention provides any T-type calcium channel (or a nucleic acid encoding such a T-type calcium channel) comprising SEQ ID NO:13 or a sequence derived from SEQ ID NO:13 having conservative amino acid substitutions, as described above.

The nucleic acid of the present invention encoding all or a part of a T-type calcium channel can be isolated via any suitable method. For example, prior to the present invention, one of skill in the art could design a probe based on the sequence of known, non-T-type, calcium channels and use such probe to screen a genetic library. If such a screen were to identify a putative calcium channel, the researcher could then attempt to clone the entire nucleic acid to characterize it. Similarly, prior to the present invention, to isolate a nucleic acid encoding a T-type calcium channel, one of skill in the art could consult publicly available databases containing DNA sequences (e.g., Genbank) to locate nucleic or amino acid sequences representing a portion of a T-type calcium channel protein or nucleic acid. However, such databases contain no sequence for a full-length T-type calcium channel or identify any sequence as a T-type channel. Such methods assume that T-type calcium channels share sufficient sequence identity with known calcium channel nucleic acids to cross-hybridize, an assumption not supported by any published report. Moreover, prior to the present invention, no partial sequence in such databases was identified as corresponding to a T-type calcium channel. Thus, prior to the present invention, the presence of partial sequences in the public DNA databases could facilitate the isolation of T-type calcium channels only with the exercise of a considerable degree of speculation on the part of the researcher.

By providing several sequences pertaining to T-type calcium channels and a comparison presenting conserved regions and domains, the present invention greatly facilitates the isolation of other nucleic acids encoding T-type calcium channels (or derivatives thereof) with much less experimentation. Thus, while any of the methods discussed above can be employed to isolate other members of this genus, preferably, a nucleic acid encoding a T-type calcium channel is isolated by probing a genetic library using a probe that hybridizes to a DNA encoding a peptide sequence contained in (or similar to) a known T-type calcium channel (e.g., SEQ ID NOs:1-12). To facilitate the isolation of a T-type calcium channel, the present invention provides an isolated polynucleotide hybridizing to a portion of the nucleic acid of the present invention encoding a T-type calcium channel (or a portion thereof). Thus, for example, the present invention includes an isolated polynucleotide hybridizing to SEQ ID NO:1-12. The isolated polynucleotide can hybridize to all or any portion of the sequence encoding the T-type calcium channel.

To isolate such a polynucleotide, any portion of a sequence encoding a T-type calcium channel can be employed as a probe to screen a genetic library, and such screening can be accomplished by standard techniques known in the art. While the probe can hybridize to any portion of such a DNA, preferably the probe is designed to hybridize to a DNA encoding a polypeptide sequence that is highly conserved among T-type calcium channels but is less conserved between the genus of T-type calcium channels and other proteins. Such peptide sequences are readily apparent from the sequence comparison set forth in Figures 1A-1E. Generally, the specificity of hybridization in a genetic screen varies depending on the length of the probe and the stringency (e.g., temperature, salt and detergent concentration, etc.) of hybridization. Stringency of hybridization is broadly classified as "high," "moderate," or "low," and the parameters of these terms are well recognized in the art (see, e.g., Sambrook et al., "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Press, 1989). The isolated polynucleotide hybridizing to a portion of the nucleic acid encoding a T-type calcium channel can hybridize under any desired stringency conditions. However, for identifying other T-type channels, preferably, the hybridization occurs under moderate stringency, and most preferably under high stringency.

Of course, the isolated or substantially purified polynucleotide can itself be employed as a probe to screen a library as described to isolate a second nucleic acid. In such a screen, one of the polynucleotides will be complementary to a portion of the sequence encoding the T-type calcium channel, and the other isolated nucleic acid will be "sense." Preferably, one of the two isolated polynucleotides (the "sense" strand) itself encodes a T-type calcium channel, or at least one domain thereof. Such a sequence can be cloned to be operably linked to suitable regulatory elements, as described, to produce a T-type calcium channel. Thus, aside from using the nucleic acid of the present invention to produce a T-type calcium channel, the nucleic acids of the present invention are also useful for isolating other sequences encoding T-type calcium channels, or derivatives thereof.

However isolated, the isolated or substantially purified nucleic acid of the present invention is useful, in part, for producing all or a portion of a T-type calcium channel. Thus, the nucleic acid can be introduced into a suitable milieu for driving its expression. Because T-type channels are transmembrane proteins, preferably such a milieu is a living cell. However, it should be understood that the nucleic acid can also be expressed *in vitro* under conditions, such as those known in the art, suitable for *in vitro* transcription and translation. However produced, the present invention includes any protein, such as a recombinant protein or an isolated or substantially purified protein, including all or a portion of a T-type calcium channel or a protein derived from a T-type calcium channel.

For expression in a living cell, the nucleic acid must be introduced into the cell. As nucleic acids are generally introduced into cells as part of genetic vectors, the present invention provides a vector having a T-type calcium channel nucleic acid of the type described above. Any type of vector suitable for introducing the nucleic acid into a host cell is within the context of the present invention. Examples of such vectors include naked DNA and RNA vectors (such as oligonucleotides, plasmids, capped cRNA, etc.), viral vectors such as adeno-associated viral vectors (Berns et al., *Annals of the New York Academy of Sciences, 772*, 95-104 (1995)), adenoviral vectors (Bain et al., *Gene Therapy, 1*, S68 (1994)), herpesvirus vectors (Fink et al., *Ann. Rev. Neurosci., 19*, 265-87 (1996)), packaged amplicons (Federoff et al., *Proc. Nat. Acad. Sci. USA*, 89, 1636-40 (1992)), papilloma virus vectors, picornavirus vectors, polyoma virus vectors, retroviral vectors, SV40 viral vectors, vaccinia virus vectors, and other vectors. Once a given type of vector is selected, its genome must be manipulated for use as a background vector, after which it must be engineered to incorporate exogenous polynucleotides. Such manipulations are known in the art.

The vectors of the present invention are useful for introducing a nucleic acid encoding all or a portion of a T-type calcium channel into a host cell. Thus, the present invention provides a cell into which the vector of the present invention has been introduced. The host cell can be any cell suitable for expressing the nucleic acid (e.g., bacteria, insect cells, mammalian cells, etc.). The host cell can thus be *in vitro* or *in vivo*. Preferably the cells do not exhibit native T-type calcium current. A preferred cell type is HEK-293 cells because they contain genetic elements that facilitate the expression of transgenes from a variety of expression vectors. For facilitating electrophysiological recordings, oocytes (e.g., *Xenopus* oocytes) are preferred, as they are large and readily handled.

The vector can be introduced into the cell in any manner suitable for the cell type and vector employed. In one embodiment, the vector can be used to prepare an RNA transcript *in vitro* (e.g., a capped cRNA) which is then introduced into the host cell by standard methods (such as injection). Such techniques are preferred when the host cells do not actively transcribe DNA (such as oocytes). In other embodiments, a DNA vector is introduced into the cell such that it is transcribed within the cell. For example, the vector can be introduced into the cell such that it forms an extrachromosomal segment of genetic material in the cell, as is the case with many types of viral vectors. Alternatively, the vector can introduce the nucleic acid into the chromosomal DNA of the host cell.

Preferably, a cell into which the nucleic acid is introduced is also able to express the nucleic acid to produce the α subunit protein. The expression of the nucleic acid can be detected by probing the cell for the presence of T-type calcium

channel mRNA, such as via Northern hybridization analysis, in situ hybridization, etc. More preferably, however, the cell is able to express the nucleic acid to produce the protein including all or a portion of a T-type calcium channel. In such cells, expression of the nucleic acid is confirmed by detecting the protein, for example, by probing cellular extracts with an antibody recognizing the protein (e.g., on a Western blot, etc.).

In the membrane of the cell producing the protein, the expressed protein contributes to the formation of a functional calcium channel. Where the protein encodes an entire α subunit, the full protein will possess some or all of the electrophysiological properties of T-type calcium channels described above. Where the protein encodes less than an entire channel α subunit (e.g., a domain), the protein will aggregate with other constituent domains in the membrane to form a functional channel. Thus, the presence of the protein can be detected by assaying the cell for T-type calcium channel activity. Indeed, assaying for channel activity serves to determine whether a nucleic acid encoding a putative calcium channel, in fact, encodes a species of T-type channel (as opposed to a member of another genus of calcium channels). For example, when large cells (e.g., oocytes) are used as the host cells, the electrophysiological properties of the channel can be investigated. Thus, the membrane activity of whole cells expressing the nucleic acid can be measured directly, such as via patch clamp techniques using a voltage clamp electrode and a current electrode (Bernal et al., *J. Pharmacol. Exp. Ther.*, *282*, 172-80 (1997)). Alternatively, the activity of single channels can be measured, such as with a standard depolarizing bath and pipette solutions (Lacerda et al., *Biophys. J.*, *66*, 183-43 (1994)). However measured, the properties of cells into which the putative nucleic acid is introduced are compared to the channel conductance, voltage dependency, activation kinetics, inactivation kinetics, or tail current known for T-type channels and discussed above. A measure of current density (e.g., pA/pF) can also be used to assess the level of gene expression in the cells, normalizing for cellular volume.

While, in accordance with the present invention, an isolated cell into which the T-type calcium channel nucleic acid has been introduced (and preferably stably expressing the nucleic acid to produce the protein) can be prepared, preferably, such transfection protocols result in a population consisting essentially of such transfected cells. For standardizing the results of many experiments, it is even more desirable to employ an established cell line consisting essentially of such cells. Preferably, for use in high throughput assays, cell lines stably expressing a T-type calcium channel exhibit a current density of at least about 40 pA/pF (e.g., at least about 45 pA/pF), such as about 50 pA/pF or even 55 pA/pF or higher. Preferably, a cell line in accordance with the present invention is able to propagate the nucleic acid through

several passages (e.g., for at least 10 passages), and, preferably, the nucleic acid is stably integrated into the chromosomes of such cells. Thus, the cell line can propagate the nucleic acid for at least 20 passages, and more preferably significantly more than 20 passages (e.g., at least about 25 passages, or even more).

Regardless of the cell system, the ability to express a T-type calcium channel nucleic acid within host cells to produce an active channel permits the channel to be further studied. In this regard, the present invention provides a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel, as herein described. The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter, the presence or absence of calcium flux in response to a change in membrane potential is assayed. Any such assay can be employed within the context of the present invention, (e.g., using labile dyes, radioisotopes (e.g., ^{45}Ca), recording electrophysiological changes in the membrane, etc.). A quick method of assaying for calcium flux is first to introduce a calcium-sensitive labile dye into the cells. For example, the dye can be one such as those that fluoresce or change color in the presence of calcium, many of which are known to those of skill in the art (e.g., Indo-1). Thereafter, the cells are exposed to a depolarizing solution containing high (e.g., about 50 mM) potassium concentration and a drug, and the reaction of the labile dye is compared to control cells. Using a labile dye affords the ability to assay many putative drugs quickly in a high throughput assay for putative drugs affecting T-type channels. For example, the initial screening can be carried out in 96 well plates. Moreover, dose-response data can be readily generated by exposing the cells to several concentrations of the same putative drug.

Once a putative drug is detected, its effect on the electrophysiology of the cell (e.g., single channel conductance, voltage dependency, activation kinetics, inactivation kinetics, and tail current of the cells) can be investigated in detail. Generally, the effect of the putative drug on T-type calcium currents is assessed by measuring the various electrophysiological parameters in the presence of various concentrations of the drugs and comparing the data to untreated (or sham-treated) control cells. Cells preferably are maintained in a continuous perfusion chamber during such experiments to facilitate changing solutions. The inventive method of identifying a drug which affects T-type calcium channels can employ any nucleic acid encoding a T-type calcium channel (or derivative thereof), such as those nucleic acids described herein. In fact, as several isoforms of T-type channel exist, the assay method can be repeated using nucleic acids encoding different isoforms to identify

drugs that preferentially target a given isoform, or drugs which affect more than one isoform of T-type calcium channels.

Aside from affording an *in vitro* assay for detecting potential therapeutic or investigative drugs targeting T-type calcium channels, the method of expressing the T-type calcium channel nucleic acid can also be used *in vivo*. For example, as mentioned, several neurological and muscular diseases or disorders have implicated mutations affecting native nucleic acids encoding T-type calcium channels. The present invention, thus, provides a method of treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid. The method involves introducing a vector having the T-type calcium channel nucleic acid into cells of a host in which native expression of the nucleic acid is deficient. Thus, for example, for treating cardiomyopathy associated with deficiencies in T-type calcium channels, the vector is introduced into myocardial cells. Similarly, for treating forms of epilepsy associated with deficiencies in T-type calcium channels, the vector is introduced into neurons (e.g., thalamic neurons). Within the target cells, the nucleic acid within the vector is expressed to produce active T-type calcium channel. By similar methods, an nucleic acid having a sequence antisense to a sequence encoding a T-type calcium channel (or a portion thereof) can be expressed within a cell. The presence of an antisense sequence can down-regulate the expression of native T-type calcium channel genes by hybridizing to T-type channel mRNA within the cell. Thus, the present invention is useful to treating disorders associated with over-expression of T-type calcium channels.

T-type channel proteins (such as whole T-type calcium channels, domains of such channels, chimeras including portions of T-type calcium channels, etc.) can be employed to generate antibodies (e.g., immunoglobulins) to T-type calcium channels. Thus, the present invention provides an isolated and substantially purified antibody molecule recognizing an epitope on a T-type calcium channel. Such antibodies can be monoclonal antibodies or polyclonal antisera. Antibodies recognizing T-type calcium channels can be used to purify the channels from cell extracts or other solutions by standard methodologies (e.g., immunoprecipitation). Moreover, depending on the location of the epitopes for the antibodies on the T-type calcium channel, the antibodies can be used to affect the channel proteins present on the surface of cells. Thus, antibodies directed to T-type calcium channels are potential reagents for studying the channels as well as for therapy.

Such antibodies can be produced by any suitable method, many of which are well known in the art. Thus, for example, the antibodies can comprise polyclonal antisera obtained from innoculated animals. Alternatively, the antibody molecules can be monoclonal antibodies obtained from a cell line (e.g., a hybridoma cell line). Thus,

the present invention provides a cell which produces such antibodies. Such a cell can be *in vitro* or *in vivo*; however, where the cell is *in vitro*, preferably it is within an established cell line consisting essentially of such cells.

Several examples are presented below to illustrate the invention. Taken together, the examples demonstrate the cloning of twelve novel proteins and their characterization as T-type calcium channel α subunits. These examples are included here for purely illustrative purposes; as such, they are not to be construed so as to limit the scope of any aspect of the invention.

Many procedures employed in the following examples are techniques routinely performed by one of ordinary skill in the art (see generally Sambrook et al., *Molecular Cloning, A Laboratory Manual*. Cold Spring Harbor Laboratory. Cold Spring Harbor, NY (1989)) and are not discussed in detail. However, some reagents and methods deserve specific description. Thus, for example, *in vitro* translation and expression were conducted as described previously (Schneider et al., *Receptors and Channels, 2*, 255-70 (1995)). *Xenopus laevis* oocytes were prepared as described previously (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). To express proteins, 10 or 30 ng of capped cRNA was injected into the oocytes in a volume of 50 nl. For single channel recording, oocytes were injected with 100 ng capped cRNA and incubated for one week prior to assay.

Cells were voltage clamped using a two-microelectrode voltage clamp amplifier as described (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). The standard bath solution contained the following: 40 mM $Ba(OH)_2$, 50 mM NaOH, 1 mM KOH, 0.1 mM EDTA, and 5 mM HEPES, adjusted to pH 7.4 with methanesulfonate. The osmolality of the 2 mM Ba^{2+} and 10 mM Ba^{2+} solutions was balanced by increasing the NaOH concentration as described (Lory et al., *J. Physiol., (London), 429*, 95-112 (1990)). Voltage and current electrodes (1.5-1.8 M tip resistance) were filled with 3 M KCl. Except as noted, data were acquired at 4 kHz using the pCLAMP system, and filtered at 1 kHz. Data were analyzed using pCLAMP software. Boltzman fits and linear regression were calculated using Prism.

EXAMPLE 1

This example demonstrates the cloning and characterization of putative T-type calcium channels.

A search of the Genbank library was conducted to identify clones identified as having some degree of homology to known calcium channel sequences. The search identified an expressed sequence tagged (EST) partial sequence in a human brain clone (H06096), which was used as a probe to screen a λgt10 cDNA library prepared

from rat brain. Successive screening of the cDNA library identified five overlapping clones which were aligned to construct an entire cDNA sequence, termed α1G.

The α1G cDNA was cloned into the pSP72™ vector and sequenced by standard computer-assisted sequencing. Using the α1G cDNA, the amino acid sequence of the α1G protein was deduced and compared to the sequences of other known calcium channel α subunits. By similar methods, homologous human (H19230 and R19524) and mouse (AA286626) EST clones were also identified and partially sequenced, and alternately spliced variants were identified. The deduced cDNA and amino acid sequences for eight full-length α1G T-type channels are set forth, respectively, as SEQ ID NOs:1-8.

A second T-type calcium channel, termed α1H, was isolated by screening a human heart cDNA library with a fragment of the α1G sequence. An alternately spliced isoform was also identified. The full-length cDNA and amino acid sequences for these α1H T-type channels are set forth, respectively, as SEQ ID NOs:9 and 10.

A third T-type calcium channel, termed α1I, was isolated by screening a rat brain cDNA library at low stringency using a fragment of the rat α1G gene. Fifty plaques were identified, many of which were not detected in a second screening. A third screening with a fragment from α1H identified two clones. Subsequent screening, and the use of the GenBank database, led to the identification of the full length rat and human cDNA and amino acid sequences, set forth at SEQ ID NOs: 11 and 12, respectively.

The α1G, α1H, and α1I amino acid sequences were compared to each other and a known calcium channel (α1E) to investigate the conservation of protein structure and function. The comparison indicates that the α1G, α1H, and α1I amino acid sequences within the putative membrane-spanning domains are about 90 % identical to each other, while the α1G, α1H, and α1I sequences are only roughly 40 % identical to the α1E clone.

Figures 1A-1E indicate this conservation between the proteins. The conservation of charged residues, particularly in the S4 domains, is consistent with the role of the α1G, α1H, and α1I proteins as ion channels. However, two of the glutamates associated with ion specificity in other calcium channels have been replaced with aspartate, suggesting altered ion selectivity. Strikingly, α1G, α1H, and α1I display only low homology to sequences linking the membrane-spanning regions within each domain, and even less homology between the intracellular loops linking domains. Notably, neither α1G, α1H, nor α1I possesses sequences known to bind β subunits or Ca^{2+} ions.

EXAMPLE 2

This example demonstrates the production of cell lines stably expressing the cloned α1G, α1H, and α1I proteins.

HEK-293 cells were transfected with either the rat α1G cDNA (SEQ ID NO:1), the human α1H cDNA (SEQ ID NO:9), or the rat α1I cDNA (SEQ ID NO:11). As a control, cells were also transfected with human α1E plus human β3 (Schneider et al., *Receptors Channels*, 2, 255-70 (1994); Murakami et al., *Eur. J. Biochem.*, 236, 138-43 (1996)). The DNA constructs included a neomycin resistance gene conferring resistance to G418. The cells were cultured under standard conditions using medium containing G418 to select for stable transformants.

Surviving clones were expanded and assayed for electrophysiological activity to determine the presence of channels within the membrane. Whole-cell currents were recorded from ruptured patches using an Axopatch 200A amplifier, Digidata 1200 A/D converter, and pCLAMP 6.0 software. Data were digitized at 2 kHz and filtered at 1 kHz or off-line. All experiments were performed at room temperature. Pipettes were made out of TW-150-6 capillary tubing (World Precision Instruments, Inc., Sarasota, FL), using a Model P-97 Flaming-Brown pipette puller (Sutter Instrument Co., Novato, CA). The internal pipette solution contained the following: 55 mM CsCl, 75 mM $CsSO_4$, 10 mM $MgCl_2$, 0.1 mM EGTA, 10 mM HEPES, pH adjusted to 7.2 with CsOH. The external Tyrodes solution was the following: 140 mM NaCl, 6 mM KCl, 2 mM $CaCl_2$, 10 mM glucose, 5 mM HEPES, pH 7.4. The recording solution contained the following: 10 mM $BaCl_2$ solution (or 2 mM $CaCl_2$), 140 mM tetraethylammonium (TEA) chloride, 5 mM CsCl, 1 mM $MgCl_2$, 5 mM glucose, and 10 mM HEPES, pH adjusted to 7.4 with TEA-OH. Under these solution conditions the pipette resistance was typically 1.5-2.5 MΩ. Cell capacitance was measured by integrating the charging current during a 10 mV hyperpolarizing pulse (holding potential -80 mV).

Using these recording techniques, values for pA/pF were obtained for each cell line, which is a measure of current density normalizing for cell size. One clone (#N2) expressed the rat α1G protein and has a current density of 42 pA/pF. Another clone (#13), expressed the human α1H protein and exhibited a current density of 53 pA/pF. Three clones (#11, #19, and #25) expressed the rat α1I protein and exhibited current densities of 40 pA/pF, 45 pA/pF, and 55 pA/pF, respectively

EXAMPLE 3

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type current-voltage relationships.

Current traces were elicited by depolarizing voltage clamp pulses of the membranes of cells. The α1G, α1H, and α1I proteins were produced in *Xenopus laevis* oocytes by linearizing the DNA vectors containing the coding sequences, and transcribing the coding sequences *in vitro* by standard methods. Oocytes were then injected with the capped RNA.

Figures 2A-2E depict data obtained from these experiments using cells injected with α1G (Figure 2A), α1H (Figure 2B), and α1I (Figure 2C) and α1E (Figure 2D). These data indicate that cells expressing α1G, α1H, and α1I exhibit T-type calcium current, while oocytes expressing α1E as well as uninjected oocytes (Figure 6A) do not.

Current voltage curves were developed using cells injected with α1G, α1H, α1I, and α1E. Figures 3A depicts such data generated in a 10 mM Ba^{2+} test solution. These data were transformed into conductance and fit with a Boltzman equation to determine the midpoint of activation ($V_{0.5}$). Gating potentials for α1G, α1H, and α1I (-38 ± 1 mV n=8, -44 mV ± 1 mV, n=10, and -31 mV ± 1 mV, n=6, respectively) were in accordance with the gating potential measured for the HEK-293 cells (-41 ± 1 mV, n=10), while α1E required significantly more positive potentials to open (-2.6 mV ± .4 mV, n=3).

To compare the characteristics with published values (Huguenard, *Ann. Rev. Physiol., 58*, 329-48 (1996)), the α1G current was recorded at varying concentrations of Ba^{2+}. As indicated in Figure 3B, in solutions containing 2 mM Ba^{2+}, $V_{0.5}$ was -46.5 mV, and the slope factor (k) was 6.6 (n=7). However, when the Ba^{2+} concentration was 40 mM, $V_{0.5}$ was recorded at -21 mV, presumably due to the results of barium on surface charge screening (see, e.g., Wilson et al., *J. Membrane Biol., 72*, 117-30 (1983)). Similar values were recorded for α1H and α1I.

These results indicate that α1G, α1H, and α1I are low-voltage activated calcium channels (i.e., from about -60 mV to about -30 mV in 10 mM Ba^{2+}).

EXAMPLE 4

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type tail current.

Tail current was measured at -90 mV after first opening the channels with a voltage step to -10 mV. The voltage-dependence of tail current in cells expressing α1G (oocytes) α1H (HEK 293 cells), and α1I (HEK 293 cells) was measured at varying test potentials. As a control, tail current was also measured from a high voltage activated channel α1E, which. Raw data from recordings data were fit with a single exponential and plotted as a function of depolarization potential (Figure 4).

These results demonstrate that the tail currents for the cloned α1G, α1H, and α1I calcium channels are voltage-dependent, consistent with known T-type calcium tail currents. Additionally, these data demonstrate that the tail current for each of the cloned channels is between about 1 ms and about 10 ms following repolarization to a membrane potential from about −80 mV to about −60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

EXAMPLE 5

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type single channel conductance.

Measurement of single channel conductance is complicated by the low probability of channel opening at negative potentials when the driving force is large. Thus, single channel conductance was measured similarly for measurements of tail currents to enhance channel opening at negative potentials. Single channels were measured with standard depolarizing bath and pipette (115 mM $BaCl_2$, 1 mM EGTA, and 10 mM HEPES, pH 7.4) solutions (Lacerda et al., *Biophys. J.*, 66, 1833-43 (1994)). Data were analyzed with TRANSIT (VanDongan, *Biophys J.*, 70, 1303-15 (1996)). Single channel amplitudes were measured by averaging the values obtained from Gaussian fits to all-points histograms of traces with openings, selected openings, or amplitude histograms of idealized openings. It has been reported that some oocytes contain a native 9 pS channel. These endogenous channels can be distinguished by their 2-fold larger current amplitudes at the potentials tested (e.g., −20 mV, $i = 0.8$ for endogenous channels as opposed to 0.4 pA for α1G). However, such endogenous channels were not detected either at the whole cell or single channel level in the oocytes tested.

Current through the main open state of each open channel was measured at each potential and plotted against each test potential. Single channel currents for several patches were then averaged and plotted as a function of test potential, wherein the slope of the plot indicated the single channel conductance. The average slope conductance of the α1G channel was measured at 7.5 ± 1.5 pS, which corresponds with the reported values for T-type calcium channels (Hugenard, *Ann. Rev. Physiol., 58*, 329-48 (1996)). Similar results were also obtained with both α1H (10.8 ± 1.4 pS). Data collected from recordings of the α1I channels indicate that they open to two distinct amplitudes. The conductance for the small amplitude α1I openings was measured at 3.9 ± 0.5 pS, while that for the large α1I openings was measured at 11.4 ± 0.5 pS).

These results indicate that the cloned α1G, α1H, and α1I proteins exhibit T-type single-channel conductance (e.g., from about 4 to about 12 pS).

EXAMPLE 6

This example demonstrates that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels.

HEK-293 cells were subjected to treatment as indicated above in Example 3, except that an experimental group of cells were exposed to a solution containing 1 μM mibefradil, a known inhibitor of T-type calcium current. As depicted in Figure 5A, the presence of mibefradil almost completely abolished T-type current in cells expressing α1G. Cells expressing either α1G or α1H were similarly treated using various concentrations of mibefradil to determine a dose-response relationship. These results, depicted in Figure 5B, demonstrate that about 50% inhibition was achieved at a mibefradil concentration of 1 μM.

All of the references cited herein, including patents, patent applications, and publications, are hereby incorporated in their entireties by reference.

While this invention has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations of the preferred embodiments may be used and that it is intended that the invention may be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications encompassed within the spirit and scope of the invention as defined by the following claims.

What is claimed is:

1. A isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α subunit.

2. The nucleic acid of claim 1, wherein said protein comprises an entire T-type calcium channel α subunit.

3. The nucleic acid of claim 2, wherein said protein comprises SEQ ID NO:13.

4. The nucleic acid of any of claims 1-3, wherein said calcium channel begins to gate from about -60 mV to about -30 mV in 2 mM Ba^{2+}.

5. The nucleic acid of any of claims 1-4, wherein said calcium channel exhibits a tail current of from about 1 ms to about 10 ms following repolarization to a membrane potential from about −80 mV to about −60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

6. The nucleic acid of any of claims 1-5, wherein said calcium channel exhibits a single channel conductance of from about 4 pS to about 11 pS in a solution with a barium ion concentration of about 100 mM.

7. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of any of claims 1-6.

8. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of claim 7.

9. The nucleic acid of claim 8 comprising a sequence encoding at least one domain of a T-type calcium channel α subunit.

10. A vector comprising the nucleic acid of any of claims 1-9.

11. A cell into which the vector of claim 10 has been introduced.

12. The cell of claim 11, which expresses said nucleic acid to produce said protein.

13. The cell of claim 11 or 12, which stably expresses said nucleic acid to produce said protein.

14. A population of cells consisting essentially of cells according to any of claims 11-13.

15. An established cell line consisting essentially of cells according to any of claims 11-13.

16. A method of identifying a drug which affects T-type calcium channels, said method comprising expressing a T-type calcium channel in a cell, exposing said cell to a putative drug, and measuring the calcium flux through the membrane of said cell in response to a change in membrane potential.

17. The method of claim 16, wherein said calcium flux is assayed by using a calcium-sensitive labile dye within said cell.

18. The method of claim 16, wherein said calcium flux is assayed by measuring the electrophysiological properties of said cell.

19. The method of claim 16, wherein said calcium channel comprises SEQ ID NO:13.

20. An isolated or substantially purified immunoglobulin recognizing an epitope on a T-type calcium channel protein.

21. A cell *in vitro* which produces the immunoglobulin of claim 20.

22. An established cell line consisting essentially of cells according to claim 21.

hCavT1a MDEEEDGAGAEESQQPR----------SPMRLMELSGAGGKRGPGSGAEKDPGSAVSKEASLPVPVEPLKSQDSEPSSWCLPTVCVCPM
rCavT1a MDEEEDGAGAEESQQPR----------SPTQLMELSGAGGKQGPGSGTEKDPGSAVSKEASLPVPVEPLKSQDSKPSSWCLRTVCVCPM
hCavT2a MTEGARRAADEYKVPLSRRPWPPCGVGGSVPGSPRGAGPRGSGSELGVPSPSEAPPAERCASLGAGEEQRVPVPPALAARTVEPCLAQTTNSPSWCLRLVCVCPM
hCavT3 MASSASPPSSSSAAA----------EPAEEPGVPVPLQPGPSPSPSPGLPEPDGRDPVPPGPLAPIAFELLRQTPSPRRWCIRNVCVCPM
rCavT3 MADSSLEPSSSAAAP----------AEPEPG---ITSQPGPRSPPPSPPGLEGTSRPVVPHPGLAPVAEFCLRQTPTSPRRWCIRNVCVCPM
I81 I82 I83
hCavT1a FERISMDLVILLRCVTLGMFFCPCEDIACDSQRCRIIQAFDSPIPAFPAVEAPVRNVVRALGIFGCKKCYLGPTWNKLDFPTVLRAKELYSDLGVNFSFAVPETV
rCavT1a FERVSMDLVILLRCVTLGMFFCPCEDIACDSQRCRIIQAFDDPIPAFPAVEAPVRNVVRALGIFGCKKCYLGPTWNKLDFPTVLRAKELYSDLGVNFSFASVPETV
hCavT2a FERVSMDLVMLMCVTLGMFFCPCEDVDQSSRCNILEAFDAPIPAFPAVEAVIRNVVRALGLFGQKCCLGPIWNKLDFPTIVVRAKRELYSLGHNVSLASLRTV
hCavT3 FECVSMDLVILLRCVTLGMYQPCDDMDCLSSRCRIMQVFDDPIFIFPFAMEMVIRMVALGIFGKKCTLGPTWNKLDFPTIVRAGAMVELYSLGIQNIRLASLRTV
rCavT3 FECVSMDLVILLRCVTLGMYQPCDDMECLSSRCRIIQVFDDPIFIFPFAMEMVIRMVALGIFGKKCTLGPTWNKLDFPTIVRAGAMVELYSLGIQNIRLASLRTV
I84 I85 IP LOOP
hCavT1a KVIRPLKAINRVPSMRILVFLLLPTLFMLGSVVLLLCFFVFPIFGIVGVQLWGALLRNRCWFLPENFSLLPILSVD-LERITQTENEDESPFICSQPRNGMGES
rCavT1a KVIRPLKAINRVPSMRILVFLLLPTLFMLGSVVLLLCFFVFPIFGIVGVQLWGALLRNRCWFLPENFSLLPILSVD-LERITQTENEDESPFICSQPRNGMGES
hCavT2a KVIRPLKAINRVPSMRILVFLLLPTLFMLGSVVLLLCFFVFPIFGIVGVQLWGALLRNRCRFLDSAFVPNNNLDYEAFSTQTENEDESPFICSSRRNGMGQK
hCavT3 KVIRPLKAINRVPSMRILVFLLLPTLFMLGNVLLLCFFVFPIFGIVGVQLWGALLRNRCRFLDSNFVPNNSLDYEAFSTQTENEDESPFICSLSSGCNGMGQ
rCavT3 KVIRPLKAINRVPSMRILVFLLLPTLFMLGNVLLLCFFVFPIFGIVGVQLWGALLRNRCRFLDSNFVPNNSLDYEAFSTQTENEDESPFICSLSSGCNGMGQ
hCavT1a CRSVPFLRGSG-----GGGPGCGLDYEAIVNVSSSNFTTCVNMNQYIYNCSAGSRNPFKGAINFDNIGIAWIAIFQVITLEGWVDIMYFWMDAMSPFNMYFIYFI
rCavT1a CRSVPFLRGSG-----GGGPGCSLDYETIVNSSSNFTTCVNMNQYIYNCSAGSRNPFKGAINFDNIGIAWIAIFQVITLEGWVDIMYFWMDAMSPFNMYFIYFI
hCavT2a CSHIPGRGVDMGPCTLDMEA-TTQPQAKGVGAASRGCINNNQYIYNVCSSGSNPHRGAINFDFNTCCAWIAIFQVITLEGWVDIMYYWLDAMSEFNNFIIYFI
hCavT3 CHEIPPLKSQGSRGCCLSKDDVYDPSAGKQGIMASSLCVWWNRIIYNVCNTGNAMPKGAINFDNIGIAGIVIVIFQVITLEGWVEIMIYVWLDAMSPFNIFYFI
rCavT3 CHEIPPLKEQGSRGCCLSKDDVYDPSAGKQGIMASSLCVWWNRIIYNVCNTGNAMPKGAINFDNIGIAGIVIVIFQVITLEGWVEIMIYVWLDAMSPFNIFYFI
I86 IP LOOP
hCavT1a LLIIVGSFFMFNLGIVVIATQFSETKQKSQLDMEFQGAVNRFLSNASTLASFSKPSGCYEELLKTLVTILHKGAAERLAQVSRAIVYVGLLSFPAFLGSQEI
rCavT1a LLIIVGSFFMFNLGIVVIATQFSETKQKSQLDMEFQGAVNRFLSNASTLASFSKPSGCYEELLKTLVTILHKGAAERLAQVSRAIGYVAAGLLSFPVASSQEP
hCavT2a LLIIVGSFFMFNLGILVVIATQFSETKQKSQLAMEFQGAANRHLSNDSTLASFSKPSGCYEELLKTVGHIFPHSVPRRSRLRLIARWGSSWSKKRVDPSAVQGQSP
hCavT3 LLIIVGSFFMFNLGVVYATQFSETKQKSHIDLEFQGVVTGSLSS-STVASTAEPSDCYEEIFPQYVCHLIRKAAERAALGGIQTAVLGSPSQ
rCavT3 LLIIVGSFFMFNLGVVYATQFSETKQKSHIDLEFQGVVTGSLSS-STVASTAEPSDCYEEIFPQYVCHLIRKAAERAALGGIQTAVLGSPSQ

Fig. 1A

Fig. 1B

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IIIP LOOP
IIIS6
hCavT1a SDCAEASYRWVFHHKTNFDNLQQALDSLFVLASKDGWVDIMVDGLDAVSVDQQPPMRNRPWMLLYITSFLILVSAFVVLSMFVGVVSENFHKCNQHQEEEA
rCavT1a SDCAEASYRWVFHHKTNFDNLQQALDSLFVLASKDGWVDIMVDGLDAVSVDQQPPMRNRPWMLLYFTSFLILVSAFVVLSMFVGVVSENFHKCNQHLCEESEA
hCavT2a AQCRAAHFRWVFHHKTNFDNLQQALDSLFVLSSKDGWVNIMVDGLDAVSVDQQPPQRPRPWMLLYITSFLILVSFFVLSMSFVGVVSENFHKCIEHKYTHQEKEEA
hCavT3 SDCMAAHFRWVFHHKTNFDNLQQALDSLFVLASKDGWVNIMVDGLDAVSVDQQPPTRHRPWMLLYFTSFLILVSGFFVLSMFVGVVSENFHSCWQHQRKEEA
rCavT3 SDCYAAHFRWVFHHKTNFDNLQQALDSLFVLASKDGWVNIMVEGLDAVAVDQQPVTRHRPWMLLYFTSFLILVSSFFVLSMFVGVVSENFHKCWQHQRKEEA
IVS1 IVS2
hCavT1a ERREEEKKLRFLKQGRQRSKEKNQWSRAQCKPVYSDVSMEPKLLVHHLCTSHVIDLFFTFGFGLMVVTMAMDHYNQPTDSLQISLDILNKVFTVMFVLEMSVKMLA
rCavT1a RRREEEKKLRFLKEQGGRSKEKNQWSRAQCKPVYSDVSMEPKLLVHHLCTSHIIDLFFTFGFGLMVVTMAMDHYNQPTDSLQISLDILNKVFTVMFVLEMSVKMLA
hCavT2a ERREEEKKLRFLKELEQGGRSKEKNQWSRAQCKPVYSDVSMEPKLLVHHLCTSHLLDLFFTFLICVNVIIMSMEHYNQPKWSSLDSALKICGVLGFLFSFLVRDLCMKVLA
hCavT3 RRREEEKKLRFLKELEQGR--R-------AQRLLFYATYCHFRLLIHHMCTSHSIDLIFIFLICLNVVTMSLEHYNQPTSLEIALKICNYFFTVFVLEAVLKLVA
rCavT3 ERREEEKKLRFLKKLEKGGR--R-------AQRLLFYATYCLFRLLIHHMCTSHSIDLIFIFLICLNVVTMSLEHYNQPTSLEIALKICNYFFTVFVLEAVLKLVT
IVS3 IVS4 IVS5
hCavT1a AFGFFRDRFNQMNQLDDLAVLLSIMSIITLEEIEVNKSLPINPTIIKIRMEVILRAVKLLRVAKVGKFSALLDTVDQALPQVGNLGLLFMLLFIFAALGVE
rCavT1a AFGFFRDRFNQMNQLDDLAVLLSIMSIITLEEIEVNLSLPINPTIIKIRMEVILRAVKLLRVAKVGKFSALLDTVDQALPQVGNLGLLFMLLFIFAALGVE
hCavT2a AFGFFRDRFNQMNQLDDLAVLLSLMSIITLEEIEMNSAALPINPTIIKIRMEVALRAVKLLRVAKVAKFSQFLNTVDQGLLGLFNLLLFIPAALGVE
hCavT3 AFGLFRDRFNQMNQLDDLAVLLSVMSITTLEEIEVNAALPINPTIIKIRMEVILRAVKLLRVAKTGKFSAALLDTVVQALPQVGNLGLLFMLLFIYAALGVE
rCavT3 AFGLFRDRFNQMNQLDDLAVLLSVMSITTLEEIEVNTALPINPTIIKIRMEVILRAVKLLRQAKTGKFSAALLDTVVQALPQVGNLGLLFMLLFIYAALGVE
IVP LOOP IVS6
hCavT1a LFGDLECDSTHPCEGLGRHAIFRSGHEARHLFDFGVFSGRNMGIGELPSQTDSERSF---GTMFVISFYIVFVSFVLVNMFVAVIMKTFEESNKQE
rCavT1a LFGDLECDSTHPCEGLGRHAIFRSGHEARHLFDFGVFSGRNMGIGELPSQTDSERSF---GTMFVISFYIVFVSFVLVNMFVAVIMKTFEESNKQE
hCavT2a LFGELECESTHPCEGLESHAIFRSGHEARQFSNFGSMSRALFLPYVSFEGDNMGIGMDTLRSEPVTEVNDPQFVNRVVVATMESLIESNKQE
hCavT3 LFSKLVCNDENPCEGMSEHAIFESNFGMSFLFLFQVSTEGGNMGIGMDTLRSECTMDERACTCLSSLQPVSSFIIFVSFVLIGMFVALMLKLFNSNYE
rCavT3 LFSKLVCNDENPCEGMSEHAIFESNFGMSFLFLFQVSTEGGNMGIGMDTLRDCTMDERACTCLSSLQPVSSFIIFVSFVLIGMFVALMLKLFNSNYE
hCavT1a AKEEAELEAELKLEKSKTLSPQHSPIGAGSFAMPGVKEGPDSRSDSLAALPPAAHAGSASWFSLEHPTMQPHPPELP----GPDLLTVPAKSGVSETHSLPND
rCavT1a AKEEAELEAELKLEKSKTLSPQPHSPIGSGSFPMPGVKEGVHSTDSRPPQAPHTTAHIGAASGGFSLEHPTPNVPGPDLLTIGVADGVSRTHSLPND
hCavT2a AKEDAELDRIELEMAQGSPDSAREV--DADRPPLPQRSPGRSDAPVLVAKVSYSPCMLSLPND
hCavT3 AQEDAERGAMSLETEEMDHDLGP--
rCavT3 AQEDAENDMSLETSLESMAHGLGPCPGPCPCPCPCPCA--

Fig. 1D

```
hCa_T1a SYMCRHGSTAEGFLGHRGWGIFGAQSGSVLSVHSQPADTSYIIQLPEGADPHLLQPHSAFTWGFTPKLPPPGKSFLAQRHLRKQAAIRTDSLDVQGLGSRE
rCa_T1a SYMCRHGSTDEESLGHRGWGLPKAQSGSILSVHSQPADTSCIIQLPKGVHYLLQPHGAFTWGAIPKLPPPGKSFLAQRPLRKQAAIRTDSLDVQGLGSRK
hCa_T2a SYMFRLPVVPASAPHPRIQEYEMETYGAGYPRLSPVASVHSPPAESCASLQIPLAVSIPARSGS-----------------------------------
hCa_T3  ----------GPRLPTGSPCAPGRGSPGAGAGGGDTDGGLCRHCTSPAQETTWLDSVSLIIKDS-----------------------------------
rCa_T3  ----------GPRLPTSSPCAPGRGSPGAGAGGDTESHLCRHCTSPAQETTWLDSVSLIIKDS-----------------------------------

hCa_T1a EALLSEVSGPSPPLLRAVSPWCQSSITQAQQHSRSHSKTSHHMTTPAPCPGPLPWWCKGAPPETRSSLELDTELSWISGDLLFPSS-QESPSPWPLKKCTSVE
rCa_T1a DLLSSEVSGPSCPLTRSSPWCQSSITQVQQPSGIQSKVSKHIKLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLFPSS-QESPSPWPLKKCTSVE
hCa_T2a ----------EHALSPRGTNPSPSLSRLLCRQEAVHTDSLAGKLTALGTPWILQSLVKKPR (SEQ ID NO:9)
hCa_T3  ----------LEGELTIIDMLSGSIFHHYSSPAGCKKCHHDKQETCGPRPSCWYTT (SEQ ID NO:11)
rCa_T3  ----------LEGELTIIDMLSGSVFHHYASPMGCKKCHHDKQETCGLRPSCWGHT (SEQ ID NO:12)

hCa_T1a AQSCQRRPTSWLDEQRRHSIAVPSCLDSGSQPHLGTDPSWLGGQPLGGPGSEPKKDLSPPSITIDPPESQQPETPPSPGCLCLRKRALPSSDSKDFIASGPPD
rCa_T1a TQSCRRRPGPWLDEQRRHSIAVPSCLDSGSQPPLCPSPSSLGGQPLAGPGSEPKKKDLSPPSITIDPPESQQSRKPGCSPGVCLRSSAPASDSKDPSVSSPLD

hCa_T1a SMAASPSPKGCVLSLSGLSSDPADLDP (SEQ ID NO:1)
rCa_T1a STAASPSPKGCTLSLSGLSSDPTMDP (SEQ ID NO:5)
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Fig. 1E

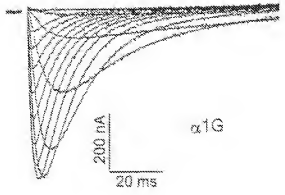

Figure 2A

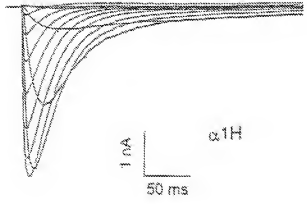

Figure 2B

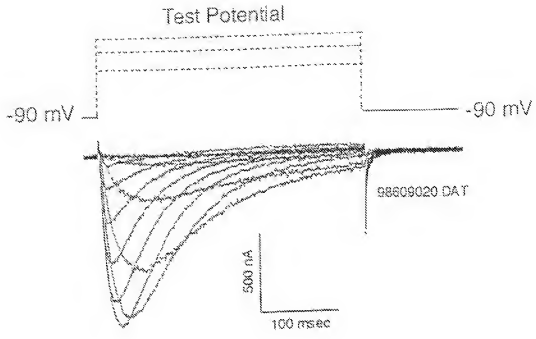

Figure 2C

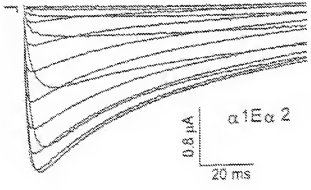

Figure 2D

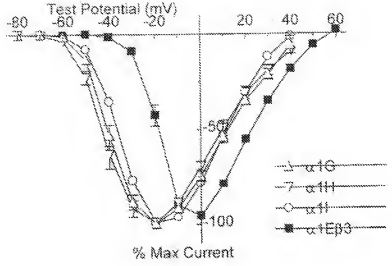

Figure 3A

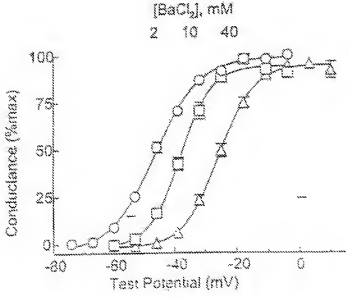

Figure 3B

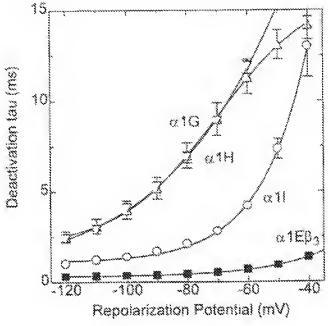
15
10
5
0
Deactivation tau (ms)
α1G
α1H
α1I
α1Eβ3
-120
-100
-80
-60
-40
Repolarization Potential (mV)

Figure 4

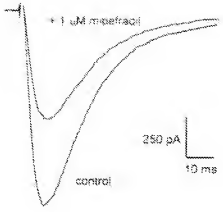

Figure 5A

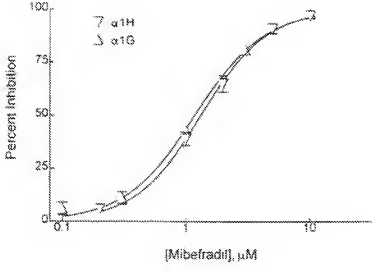

Figure 5B

SEQUENCE LISTING

<110> Perez-Reyes, Edward
Cribbs, Leanne L.
Loyola University of Chicago

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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg  144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc acg gtg gtt ttc ttc tac ttg  192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc agc cgc ccg agg agc tgg tgt ctc cgc acg acg gtc tgt aac  240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg  288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

acc ctg ggc atg ttc cgg ccc tgc gag gac atc gcc tgt gac tcc cag  336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttc gcc ttc ttt  384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gcc atg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa  432
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Ala Val Glu Met Val Val Lys Met Val Asn Leu Gly Ile Phe Gly Lys
 130                 135                 140

agg tgt tac ctg gaa gac aac tgg aac cgg ctt gac ttt ttc atc gtc  480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac atg cag aac gtc agc ttc  528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcg gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gac att aac  576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agt atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg  624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc  672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga  720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc cta cct gag aat ttc agc ctc aac ctg agc gtg gac ctg gag  768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Asn Leu Ser Val Asp Leu Glu
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cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc  816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
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cag acc cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg  864
Gln Thr Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc  912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac  960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gac atc aac 1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Asp Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg 1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc 1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aat ttc atc tac ttc atc ctc ctc atc atc grg ggc tcc ttc 1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380

ttc atg atc aac ctg tac ctg gtg gtg atc gcc acg cag ttc tca gag 1200
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Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aag cag ggg gaa agc cag ctg atg cgg gag cag cgc gtg cgg ttc  1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc  1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc  1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cgc agg ctg gct cag gtc tct cgg gca gcc ggt gtg cgg gtt ggg ctg  1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
    450                 455                 460

ctc agc agc cca gca cac ctc ggg ggc cag gag acc cag ccc agc agc  1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465                 470                 475                 480

agc tgc tct cgc rcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac  1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc  1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg  1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tcc agc agg ctc atg ctg gca ccs ccc tcg acg cct gcc atc tcc ggg  1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
    530                 535                 540

gcc ccc cct ggt ggc gca gag tct gtg cac aac ttc tac cat gcc gac  1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Asn Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca  1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
                565                 570                 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc  1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta  1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
        595                 600                 605

gag gtg gct cgc agc tct ggg ccc cca acc ctg acc agc ctc aac atc  1872
Glu Val Ala Arg Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
    610                 615                 620

cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt  1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

aca ggt gcc tgc caa agc tct tgc aay atc tcc agc cct tgc ttg aca  1968
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Thr Gly Ala Cys Glu Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
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gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tct ggt ggg  2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Gly Arg
            660                 665                 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa agg cct gac tca  2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
        675                 680                 685

gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac  2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gac ccc cac agc cgg cga cgg caa cgg agc ctg ggc cca gat  2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705                 710                 715                 720

gag ccc agc tct ggg ctg gcc ttc tgg agg cta atc tgt gac acc ttc  2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                725                 730                 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc  2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
            740                 745                 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc  2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
        755                 760                 765

gag gag ctt acc aac gcc cta gaa atc agc aac atg gtc ttc acc agc  2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    770                 775                 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt  2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785                 790                 795                 800

ggc tac atc aag aat ccc tac acc atc ttc gat ggt gtc att gtg gtc  2448
Gly Tyr Ile Lys Asn Pro Tyr Thr Ile Phe Asp Gly Val Ile Val Val
                805                 810                 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg  2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
            820                 825                 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg  2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
        835                 840                 845

cag gcg ctg cag cgg cag ctg gtg gtc atg aag acc atg agc acc cgg  2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    850                 855                 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc ggc  2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865                 870                 875                 880

atc ctg ggc atg cat ctc ttc ggc tgc aay ttt gcc tct gag cgg gat  2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                885                 890                 895

ggg gac acc ctg cca gac cgt aag aat ttt gac tcc ttg ctc tgg gcc  2736
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Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
            900                 905                 910

atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aat aaa gtc  2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
        915                 920                 925

ctc tac aat ggt atg gcc tcc acg tcg ttc tgg gcg gcc ctt tat ttc  2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                 935                 940

att gtc ctt atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc  2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc  2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat tta ttt tca ccc agc ctg gat ggt gat ggg gac  2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aaq aag tgc ttg gcc ttg gtg tcc ctg gga gag cac gcg gag ctg  3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Ala Glu Leu
        995                 1000                1005

ggg agg agc ctg ctg cag cat ctc atc atc cac acg gcc gcc aca ccc  3072
Arg Arg Ser Leu Leu Gln His Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg atg aac aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc  3120
Met Ser Met Asn Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc aac agc agc agc ggg tcg gca gag cct ggg gag  3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac aag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc  3216
Ala His Lys Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agt ccg aac  3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Pro Asn
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agc ctc ggc cgt gca ccc agc ctg aag ccg aga agc cca agt gga gag  3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag  3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
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gag agc tca gaa gag gag ccg gcc agc cct gcg ggc agt gac cat cgc  3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135

aac aag ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca  3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150

gac aca ctg cag ctg cca ggg ctg cac cgc act gcc agt ggc cga ggg  3504
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Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
1155 1160 1165

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Ser Ala Ser Glu His Gln Ala Cys Asn Gly Lys Ser Ala Ser Val Arg
1170 1175 1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac 3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185 1190 1195 1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg 3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
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atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca 3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
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gcc tac atc ttc cct cct cag tga agg ttc cgc ctc ctg tgt cac cgg 3744
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1235 1240 1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc acc ttc 3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
1250 1255 1260

aat aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac 3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265 1270 1275 1280

agc gct gaa cgc atc ttc ctg acc ctc tac aat tac atc ttc acc gca 3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Tyr Asn Tyr Ile Phe Thr Ala
1285 1290 1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc 3936
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Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
1330 1335 1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg 4080
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cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag 4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
1365 1370 1375

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Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
1380 1385 1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg 4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
1395 1400 1405

cag ctc ttc aaa ggg aag ttt ttc ctg tgc cag ggc gag gat acc agg 4272

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Glu Leu Phe Lys Gly Lys Phe Pro Val Cys Gln Gly Glu Asp Thr Arg
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aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc  4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg  4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                1445                1450                1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg  4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc  4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc gtg ctc att gtg gcc ttc ttt  4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt  4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag gag gaa gag cag gcc cgg cgg cgg gag gag aag cgc  4608
Arg Gln His Gln Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

ctg cgg agc ctg gag aac aag aga agg agt aag gag aag cag atg gct  4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
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gag gcc cag tgc aaa cct tac tac ttc gac tac tcc agg ttt cgg atc  4704
Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyx Ser Arg Phe Arg Leu
        1555                1560                1565

ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc atc aca  4752
Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr
    1570                1575                1580

ggt gtc ttc ggg ctg aac gtg gtc acc atg gcc atg gag cac tac cag  4800
Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln
1585                1590                1595                1600

cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac atc ttc  4848
Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe
                1605                1610                1615

act gtc atc ttt gtc ttg gag tca gtt ttt aaa ctt gtg gcc ttt ggt  4896
Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly
            1620                1625                1630

ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg gcc att  4944
Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile
        1635                1640                1645

gtg ctg ctg tac atc atg ggc atc acg ctg gag cac atc gag gtc aac  4992
Val Leu Leu Tyr Ile Met Gly Ile Thr Leu Glu His Ile Glu Val Asn
    1650                1655                1660

gcc tcg ctg ccc atc aac ccc acc atc atc cgc atc atg agg gtg ctg  5040
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Glu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Leu Met Arg Val Leu
1665                1670                1675                1680

cgc att gcc cgc gtg ctg aag ctg ctg aag atg gct gtg ggc atg cgg      5088
Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg
                1685                1690                1695

gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg      5136
Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu
            1700                1705                1710

gga ctt ctc ttc atg ttg ttg ttt ttc att ttt gca gct ctg ggc gtg      5184
Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val
        1715                1720                1725

gag ctc ttt gga gac atg gag tgt gac gag aca aac ccc tgt gag ggc      5232
Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly
    1730                1735                1740

ctg ggc cgt cat gcc acc ttt ggg aac ttt ggc atg gcc ttc cta aac      5280
Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr
1745                1750                1755                1760

ctc ttc cga gtc tcc acg ggt gac aat tgg aat ggc att atg cag gac      5328
Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp
                1765                1770                1775

acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg gtc atc      5376
Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile
            1780                1785                1790

tcg cct atc tac ttt gtg tcc ttt gtg ctg acg gcc cag ttc gtg cta      5424
Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu
        1795                1800                1805

gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag cag agc aac      5472
Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn
    1810                1815                1820

aag gag gcc aag gag cag gcc gag ctg cag cag gct gag ctg gag ctg      5520
Lys Glu Ala Lys Glu Gln Ala Glu Leu Gln Gln Ala Glu Leu Glu Leu
1825                1830                1835                1840

atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc ccc ttc      5568
Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe
                1845                1850                1855

ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc aag cct      5616
Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro
            1860                1865                1870

ggg gct ctg cac cca ggg ggc cac gcg aga tca gcc tcc cac ttt tac      5664
Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His Phe Ser
        1875                1880                1885

ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca gga cca      5712
Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro
    1890                1895                1900

gac tta ctg act gtg cgg aag tct ggg gtc agc cga atg cac tct ctg      5760
Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
1905                1910                1915                1920

ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag ggg ccc      5808
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Pro Asn Asp Ser Tyr Met Cys Arg His Gly Gln Thr Ala Glu Gly Pro
            1925                1930                1935

ctg ggc tac agg ggc tgg ggg ctc cgc aaa gct cag tca ggc tcc gtc      5956
Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val
        1940                1945                1950

ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg cag ctt      6004
Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu
    1955                1960                1965

ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca acc tgg      6052
Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro Thr Trp
1970                1975                1980

ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg gct cag      6000
Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
1985                1990                1995                2000

agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg gac gtt      6048
Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
                2005                2010                2015

cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt agg ccc      6096
Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro
            2020                2025                2030

tcc ccg ccc ctg gcc cgg gcc tac tat ttt tgg ggc cag tca agt acc      6144
Ser Pro Pro Leu Ala Arg Ala Tyr Tyr Phe Trp Gly Gln Ser Ser Thr
        2035                2040                2045

cag gca cag cag cac tcn cgc agc cac agc aag atc tcn aag cac atg      6192
Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys His Met
    2050                2055                2060

acc ccg cca gcn ccc tgc cca ggc cca gaa ccc aac tgg ggc aag ggc      6240
Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly
2065                2070                2075                2080

cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg agc tgg      6288
Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
                2085                2090                2095

att tca gga gac ctc ctg ccc act ggc ggc cag cag gag acc cca tcn      6336
Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser
            2100                2105                2110

cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc tgc cag      6384
Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln
        2115                2120                2125

ggc agg cct acg tcc tgg ctg gat gag cag agg aga aac ttt atc gcc      6432
Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg Asn Phe Ile Ala
    2130                2135                2140

gtc agc tgc ctg gac agc ggn ttc cca ccc cac ctg ggc aca gac ccn      6480
Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro
2145                2150                2155                2160

tct aac ctt ggg ggc cag cct ctt ggg ggg cct ggg agc cgg ccc aag      6528
Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys
                2165                2170                2175

acc aaa ctc agc acg cct agt atc acc ata gac ccc ccc gag agc caa      6576
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Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Trp Gln Ser Gln
            2195                2185                2190

ggt ccc ggg acc ccg ccc agc ctt ggt atc tgc ctg cgg agg agc gcc   6624
Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala
        2195                2200                2205

ccg tcc agc gac tcc aag cct ccc ttg gcc cct ggc ccc cct gac agc   6672
Pro Ser Ser Asp Ser Lys Pro Pro Leu Ala Ser Gly Pro Pro Asp Ser
    2210                2215                2220

atg gct gcc tcg tcc tcc tcc aag aaa gat gtg ctg agt ctc tcc ggt   6720
Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly
2225                2230                2235                2240

tta tca tat gac cca gca gac ctg gac ccc                           6750
Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30

ggg ccg ggg tca gcm gan aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg ccg ctg gcc ccg gtg gtt ttc ttc tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc agm agg cgg agc tgg tgt ctc cgc acg gtc tgt aac   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg   288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

acc ctg ggc atg ttc cgg ccc tgc gag gac atc gcc tgt gac tcc cag   336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt   384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

ytm gtg gag atg gtg gcg aag atg gag gcc ttg ggc atc ttt ggg aaa   432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
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                130                 135                 140

aag tgt tat ctg gga gac att tgg aac cgg ctt gac ttt ttc atc gtc   480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc ggc ttc   528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Gly Phe
                165                 170                 175

tca gct gtc agg acg gtc cgt gtg ctg cga ccg ctc agg gcc att aac   576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg aag ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg   624
Arg Lys Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

ccc atg ctg ggc aac gtc ctg ctg atc tgc ttc ttc gtc ttc ttc atc   672
Pro Met Leu Gly Asn Val Leu Leu Ile Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca gag ggg ctg ctt cgg aac   720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Glu Gly Leu Leu Arg Asn
225                 230                 235                 240

tgc tta cta cct gag aat ttc agc atc ccc ctg agc gtg gac ctg gag   768
Cys Leu Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

aga tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc acc   816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cca cgc gag aac ggc atg cgg tcc tgc agg agc gtg ccc acg ctg   864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgc ggg gac ggg ggc ggt ggc ccg cct tgc ggt ctg gac tat gag gcc   912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac   960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tca gcg ggg cag cac aac ccc ttc aag ggc gcc atc aac  1008
Thr Asn Cys Ser Ala Gly Gln His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atg gcc atc ttc cag gtc atc acg  1056
Phe Asp Asn Ile Gly Tyr Ala Trp Met Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc arg tac ttt gtg arg gat gct cat tcc  1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aat ttc atc tac ttc atc ctc ctc gtc atc gtg ggc tcc ttc  1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380

ttc atg atg aac ctg tgc ctg gtg gtg gtg att gcc acg cag ttc tca  1200
Phe Met Met Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
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acc aag cat cgg gaa gac cag ctg atg cgg gac cag cgt gtg cgg ttc 1240
Thr Lys Gln Arg Glu Asp Gln Leu Met Arg Asp Gln Arg Val Arg Phe
405 410 415

ctg tcc aac gtt agc agc ctg gct agc ttc tct gag ccc ggc agc tgc 1288
Leu Ser Asn Ala Ser Ser Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
420 425 430

tat gag gag ctg ctc aag tac atg gtg tac atc ctt cgt aag gca gcc 1336
Tyr Glu Glu Leu Leu Lys Tyr Met Val Tyr Ile Leu Arg Lys Ala Ala
435 440 445

ggc agg ctg gct cag ctc tct cgg gca gca ggt gtg cgg gtt ggg ctg 1384
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
450 455 460

ctc agc agc cca gga ccc ctc ggg ggc aag gag acc cag ccc agc agc 1432
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465 470 475 480

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Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
485 490 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc 1528
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
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agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg 1576
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
515 520 525

tcc agc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctg tac ggg 1624
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac 1672
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560

tgc cac tta gag cca gtc agc tgc cag gcg ccc cct ccc agg tcc cca 1720
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
565 570 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc aac 1768
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590

gtg cac aac agc cct cca ccg gag acg ctg aag gag aag gca cta gta 1816
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605

gag gtg gct gac agt tct ggg ccc cca acc ctc acc agc ctc aac atc 1864
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620

aca ccc ggg ccc tac agt tca arg cac aag ctg cta gag aca cag agt 1912
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640

aca ggt gac tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa 1960
Thr Gly Asp Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys

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                    625                 630                 635

gcd gac agt aga gcc tgt ggt tcc gac agc tgc ccc tac tgt gcc cgg  2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            640                 645                 650

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca  2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
        655                 660                 665

gac agc gag gcs gtt tct gag ttc acs cag gat gcc cag cac agc gac  2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    670                 675                 680

ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca  2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
685                 690                 695                 700

gag ccc agc tct gtg ctg gcc ttc tgg agg cbc atc tgt gac acc ttc  2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                705                 710                 715

cga aag ctt gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc  2256
Arg Lys Leu Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
            720                 725                 730

atc ctg gtc aac acs ccc agc atg ggc atc gag tcc cac gag cag ccc  2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
        735                 740                 745

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc  2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    750                 755                 760

ttc ttt gcc ctg gag atg ctg ttg aag ctg ctt gtg tat ggt ccc ttt  2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
765                 770                 775                 780

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc  2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                785                 790                 795

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggg ctg tcy gty  2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
            800                 805                 810

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg  2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
        815                 820                 825

ccg gtg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac  2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    830                 835                 840

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc  2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
845                 850                 855                 860

atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tat gag cgg gat  2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                865                 870                 875

ggg gac acc ctg ccc gac agg aag act ttt gac tcc ttg ctc tgg gcc  2736
Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
            880                 885                 890
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atc gtc act gtc ttt cag atc ctg acc tcg gag gat tgg aac aaa gtt  2784
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        915                 920                 925

ttc tac aac ggt ctg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc  2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                 935                 940

att gcc ctc atg acc ttc ggc aac tac gtg ctt tcc aat ttg ctg gtc  2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc  2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat ttt ttc tca cac agc ctg gat ggt gat ggg gac  2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg  3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
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ccg aag agc ctg ctg cag cct ctc atc cac acg gcc gcc aca ccc  3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg cgc gag gcg ctg ggc  3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc aac agc agc agc ggg tcg gca gag cct ggg gcg  3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc  3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac  3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
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agc ttc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag  3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag  3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc  3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135

cac agg ggg tcc ctg gag cga gag gcc aag agt tcc ttt gac ctg cca  3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150

gac aca ctg cag gtg cca ggg ctg cat cgc aat gcc agt ggc cga ggg  3504
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
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                1155                1160                1165

tct gat tcc gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgt  3552
Ser Ala Ser Glu His Glu Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
    1170                1175                1180

ctg gcc cgg gcc ctg cgg cct gat gac cac cca ctg gat ggg gat gac  3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185                1190                1195                1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg  3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                1205                1210                1215

atc cga gcc aga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca  3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
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gac tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg  3744
Asp Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
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atc atc aac cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc  3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
    1250                1255                1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac cca cac  3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265                1270                1275                1280

agc gat gaa cgc ctc ttc ctg acc ctc tcc aat tac atc ttc acc gca  3888
Ser Asp Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                1285                1290                1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc  3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
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ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg  3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
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ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct  4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
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gac agc ggc acc aag atc ctg ggc aag ctg agg gtg ctg cgg ctg ctg  4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
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cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag  4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                1365                1370                1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggt aac atc  4176
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
            1380                1385                1390

gtg gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg grg  4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
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Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
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Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg aac aag tac aac ttc gac aac ctt cac cag gcc ctg atg tcc ctg   4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
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ttc gtt tcg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg   4416
Phe Val Ser Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
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ctg gat gct gtg ggc gtg gac cag tac ccc att atg aac cac aac ccc   4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
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tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt   4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
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gtc ctg aac atg ttt gtg ggt gtg grg grg gag aac ttc cac aag tgt   4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
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agg cag cac tag gag gaa gag gag gcc cgg agg cgg gag gag aag cgc   4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

ctg cga aga ctg gag aaa aag aga agg aat ctg atg ctg gag gat gta   4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp Asp Val
            1540                1545                1550

att gct tcc ggc agc tca gac agc gct gcg tca gaa gcc cag tgc aaa   4704
Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln Cys Lys
        1555                1560                1565

cct tac tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg   4752
Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
    1570                1575                1580

tgc acc agc cac tac ctg gac ctc ttc atc ana ggt gtc atc ggg ctg   4800
Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
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aac gtg gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg   4848
Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
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gat gag gcc ctg aag atc tgc aac tac atc ttc acc gtc atc ttt gtc   4896
Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
            1620                1625                1630

ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc   4944
Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
        1635                1640                1645

cag gac agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc   4992
Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
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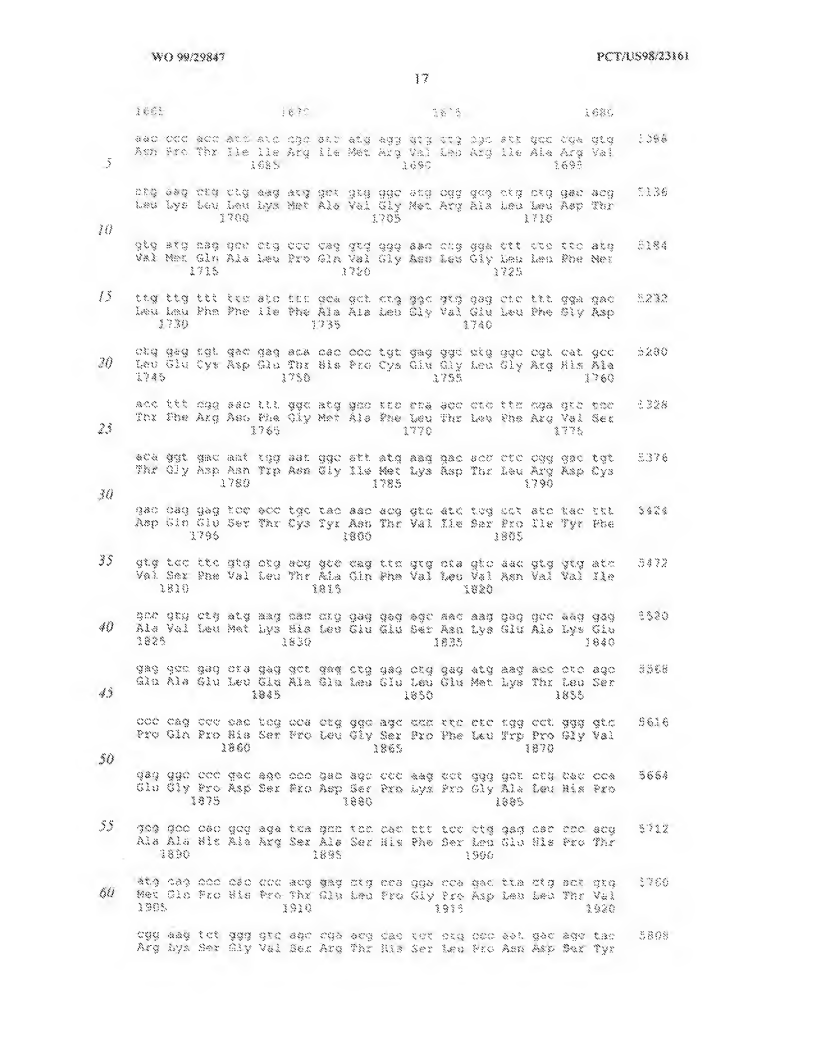
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Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
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Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
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Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
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gcc gtg ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag 5520
Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
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gag gcc gag ctg gag gct gag ctg gag ctg gag atg aag acc ctc agc 5568
Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
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ccc cag ccc cac tcg cca ctg ggc agc cgc ttc ctc tgg cct ggg gtc 5616
Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
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Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro
1875 1880 1885
gcg gcc cac gcg aga tca gac tac cac ttt tcc ctg gag cac ccc acg 5712
Ala Ala His Ala Arg Ser Asp Tyr His Phe Ser Leu Glu His Pro Thr
1890 1895 1900
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Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val
1905 1910 1915 1920
cgg aag tct ggg gtc agc cgg acg cac tct ctg ccc act gac agc tac 5808
Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Thr Asp Ser Tyr

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atg tgt cag cat ggg agc act gtc gag ggg ccc ctg gga cac agg ggc  5856
Met Cys Arg His Gly Ser Thr Val Glu Gly Pro Leu Gly His Arg Gly
        1940                1945                1950

tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc  5904
Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser
    1955                1960                1965

cag cca gcc gat acc agc tac atc ctg cag ctt ccc aaa gat gca ccc  5952
Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro
1970                1975                1980

cat ctg ctc cag cac aac agc agc aca acc tgg ggc acc atc acc aaa  6000
His Leu Leu Gln His Asn Ser Ser Thr Thr Trp Gly Thr Ile Thr Lys
1985                1990                1995                2000

ctg ccc cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc  6048
Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg
                2005                2010                2015

cag gca gca atg agg act gac tcc ttg gac gtt cag agt ctg ggc agc  6096
Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Ser Leu Gly Ser
            2020                2025                2030

cgg gaa gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc  6144
Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala
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ggg gcc tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac  6192
Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His
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tcc cgc agc cac agt aag atc tcc aag cac atg acc ccg cca gcc cct  6240
Ser Arg Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro
2065                2070                2075                2080

tgc cca ggc cca gaa ccc aac tgg ggc aag ggc cct ccg cag acc aga  6288
Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg
                2085                2090                2095

agc agc tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc  6336
Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu
            2100                2105                2110

ctg ccc cct ggc ggc cag gag gag atc tca tcc cca cgg gac ctg aag  6384
Leu Pro Pro Gly Gly Gln Glu Glu Ile Ser Pro Arg Asp Leu Lys
        2115                2120                2125

aag tgc tac agc gtg gag gcc cag agc tgc cag ccc cgg cct acg tcc  6432
Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Pro Thr Ser
    2130                2135                2140

tgg ctg gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac  6480
Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp
2145                2150                2155                2160

agc ggc tcc cag ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc  6528
Ser Gly Ser Gln Pro His Leu Gly Thr Arg Pro Ser Asn Leu Gly Gly
                2165                2170                2175

cag cct ctt ggg ggg cct ggg agc cgg ccc aag aag aaa ctt agc ccg  6576
Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro
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                2190                2195                2200

ccc ggt atc acc ata gac ccc ccc gag agc cag ggt ccc agg acc ccg   6624
Pro Gly Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro
        2205                2210                2215

gcc agc cct ggt atc tgc ccc cgg agg agg gct ccg tcc agc gac tcc   6672
Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser
    2220                2225                2230

aag gat ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc   6720
Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro
2235                2240                2245

tca gca aag aaa gat gtg ctg agt ctc ccc ggt tta tcc tct gac gca   6768
Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro
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gca gac ctg gac ccc                                              6783
Ala Asp Leu Asp Pro
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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
  1               5                  10                  15

cgg agc ttc atg cgg ctc aac gac ctg tcg cgg gcc ggg ggg cgg cgc    96
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc agc ccg ccg agc tgg tgt ctc agc acg ccg gcc tgt   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccc tgg ttt gag cgc atc agc atg ctg gtc atc ctt ctc ctg aac tgc   288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

acc ctg ggc atg ttc agg ccc tgt gag gac atc gcc tgt gac tcc cag   336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag aca gcc ttt gac gac ttc atc gcc acc ttc   384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125
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gcc gtg gag atg gtg gtg agg atg gtg gcc ttg ggc atc ttt ggg aaa  432
Ala Val Glu Met Val Val Arg Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aag tgt ttc ctg ggg gac act tgg aac cgg gtt gat ttt ttc atc gcc  480
Lys Cys Phe Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg ctg gag tac tgt ctg gac ctg tcg cag aac gtc agc ttc  528
Ile Ala Gly Met Leu Leu Glu Tyr Cys Leu Asp Leu Ser Gln Asn Val Ser Phe
                165                 170                 175

tca gct gtc agg acg gtc cgt gtg ctg cga ccg ctc agg gcc ata aac  576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ctc agc atg cgc atc ctt gtc acg ttg ctg ctg tct gat acg ctg  624
Arg Val Leu Ser Met Arg Ile Leu Val Thr Leu Leu Leu Ser Asp Thr Leu
        195                 200                 205

ccc atg ctg ggc aac gtc ttg ctg ctc tgc ttc ttc gtc ttc ttc atc  672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga  720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gat ctg gag  768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cgc tat tac cag acg gag aac gag gat gag agc ccc ttc atc tgc tcc  816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg  864
Glu Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
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cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc  912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac  960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

atc cac tgc tca gcg ggg gag cac aac gcc ttc aag ggt gcc atc aac  1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg  1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
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ctg gag ggc tgg gtc gac atc atg tac tat gtg atg gat gcc cat tcc  1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Tyr Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aat ttt atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc  1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380
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Phe Met Ile Asn Leu Ser Leu Val Val Ile Ala Thr Glu Phe Leu Gly Glu
385                 390                 395                 400

acc aag cag cgg gaa agc ctg atg ctg cgg gag cag cgt gtg cgg ttc      1248
Thr Lys Gln Arg Glu Ser Leu Met Arg Gln Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aac gcc agc acc ctg gtt agt tct gag ccc ggc agc tgc      1296
Leu Ser Asn Ala Ser Thr Leu Val Ser Phe Ser Gln Pro Gly Ser Cys
            420                 425                 430

tat gag gag ctg ctc aag tcc ctg tac atc ctt cgt aag gca gcc      1344
Tyr Glu Glu Leu Leu Lys Ser Leu Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg      1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
    450                 455                 460

ctc agc agc cca gca ccc ctc ggg ggg cag gag acc cag ccc agc agc      1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465                 470                 475                 480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac      1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cac cac cac cat cac cac cac tac tac ctg ggc aat ggg acg ctc      1536
His His His His His His His His Tyr Tyr Leu Gly Asn Gly Thr Leu
            500                 505                 510

agg gcc ccc agg gcc agc ccg gag atc cag gac agg gat gcc aat ggg      1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

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Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
    530                 535                 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac      1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

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Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
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tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc      1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
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gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta      1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
        595                 600                 605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ccc aac atc      1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Pro Asn Ile
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cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt      1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
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acc ggt gcc tgc caa agc tcc tgt aag gtc tcc tgc tcc tgc ttg aaa  1969
Thr Gly Ala Cys Gln Ser Ser Cys Lys Val Ser Cys Ser Cys Leu Lys
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gca gac agt gga gcc tgt ggc ccg gac agc tga ccc cac tgt gcc cgg  2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca  2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
        675                 680                 685

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Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gac ccc cac agc agg agg caa cgg agc ctg ggc tca gat gca  2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705                 710                 715                 720

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Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
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cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc  2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
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atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc  2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Gln Gln Pro
        755                 760                 765

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc  2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    770                 775                 780

ctc ttt gcc ctg gag atg ctg cng aag ctg ctt gtg tat ggt acc ttt  2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785                 790                 795                 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc  2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                805                 810                 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ctg tcg gtg
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Leu Ser Val
            820                 825                 830

ctg cgg acc ttc cgc atg atg cgt gtg ctg aag ctg gcg cgc ttc ctg  2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
        835                 840                 845

ccg gcg ctg cag cgg cag ctg gtg gtc atg aag acc atg gac aac  2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    850                 855                 860

gtg gcc aac acc tgc atg ctg ctt atg atc ttc atc ttc ttc atc agc  2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865                 870                 875                 880

atc ctg ggc atg cac ctc ttc ggc tgc aag ttt gcc tit gag gag gat  2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                885                 890                 895
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ggg gac atc ctg cca gac cgg aag aat ttt gat tat ttg ctt ggg gcc  3736
Gly Asp Ile Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
        900                 905                 910

atc gtc att gtc ttt gag gtc ctg gac cag gag gac tgg aac aaa gtc  3784
Ile Val Ile Val Phe Glu Val Leu Asp Gln Glu Asp Trp Asn Lys Val
    915                 920                 925

ctg tac tac ggt gtg ggc tcc acg tcg tcc tgg gcg gtt gtt tat ttc  3832
Leu Tyr Tyr Gly Val Gly Ser Thr Ser Ser Trp Ala Val Val Tyr Phe
930                 935                 940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttt aat ttg ctg gtc  3880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag ggc gat gcc aac aag tcc  3928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac  3976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg  4024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                 1000                1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca cct  4072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc  4120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gag tcg cgc ngc acc agc agc agc ggg tcg gca gag cct ggg gcg  4168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc ngc agc ncr ccg cac agc  4216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc kgg agc gcc gca agc agc tgg acc agc agg cgc tcc agc cgg aac  4264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
        1075                1080                1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag  4312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg tcg tcg gga gaa ggc nag gag agc cag gat gaa gag  4360
Arg Arg Ser Leu Ser Ser Gly Glu Gly Xaa Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cct cgc  4408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135

cac agg ggg tcc ctg gag cgg gag gcc aag agt tct ttt gac ctg cca  4456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150
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gac aca ctg cag gtg atc ggg ctg gac ctc acc gcc agt ggc tgg ggg   3504
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
        1155                1160                1165

tct gct tct gag cac tag gac tgc aat ggc aag tcg gct tca ggg cgc   3552
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
    1170                1175                1180

ctg gcc cgg gcc ctg ggg cct gat gac ccc cta ctg gat ggg gat gac   3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185                1190                1195                1200

gcc gat gac gag ggc aac ctg agc aaa ggg gac cgg gtc cgc ggg cgg   3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                1205                1210                1215

atc cga gcc cga ctt cct gcc tgc tgc ctc gag cga gac tcc tgg tca   3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
            1220                1225                1230

gcc tac atc ttc cct ccc cag tcc agg ttc cgc ctc ctg tgt cac cgg   3744
Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
        1235                1240                1245

atc atc acc aac aag atg ttc gac cac gtg gtc ctt gcc atc atc ttc   3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
    1250                1255                1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac   3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265                1270                1275                1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca   3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                1285                1290                1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc   3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
            1300                1305                1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg   3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
        1315                1320                1325

ctg ttg gtg ctc atc tcc ttc atc gac att ctg gtg tcc atg gtc tct   4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
    1330                1335                1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg   4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
1345                1350                1355                1360

cgg atc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag   4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                1365                1370                1375

ctg gtg gtg gag acg ctg atg tcc tta ctg aaa ccc atc ggc agc att   4176
Leu Val Val Glu Thr Leu Met Ser Leu Leu Lys Pro Ile Gly Ser Ile
            1380                1385                1390

gta ctc atc tgc tgt gcc tcc ttc atc att ttc ggc atc ttg ggg gtg   4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
        1395                1400                1405
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cag ctc ttc aaa ggg aag ttt ttc gtg tgt cag ggc gag gat gcc agg      4272
Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
    1415                1420                1425

aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tat cgg tgg gtc      4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1430                1435                1440

agg cac agg tac aag ttc gac aac atc ggc cag gcc atg atg tcc ctg      4368
Arg His Arg Tyr Lys Phe Asp Asn Ile Gly Gln Ala Met Met Ser Leu
                1445                1450                1455

ttc gtc ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg      4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gcc gtg ggc gtg gac cag cag ccc atc acg aac cac aac ccc      4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt      4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt      4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag cag gag gaa gag cag gcc cgg cgg cgg gag gag aag cgc      4608
Arg Gln His Gln Gln Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

ctg cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct      4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
            1540                1545                1550

gat ctg atg atg gac gat gta att gct tcc ggc agc tca gcc agc gct      4704
Asp Leu Met Met Asp Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala
        1555                1560                1565

gcg tca gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc      4752
Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
    1570                1575                1580

agg ctc ctc gtc cac cac ttg tgc acc agc cac tac ctg gac atg ttc      4800
Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
1585                1590                1595                1600

atc acg ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac      4848
Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
                1605                1610                1615

tac cag cag ccc cag att ctg gat gag gct ctg aag atc tgc gac tac      4896
Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
            1620                1625                1630

atc ttc act gtc ttc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc      4944
Ile Phe Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala
        1635                1640                1645

ttt ggt ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gat ctg      4992
Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
    1650                1655                1660
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gcc att gtg ctg ctg tcc atc atg ggc atc aag ctg gag gac atc gag 5040
Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Asp Ile Glu
1665 1670 1675 1680

gtg aac gcc agg ctg tcc atc aac ccc acc atc acc cgc atc agg 5088
Val Asn Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
1685 1690 1695

grg ctg cgc act gcc cga gtg ctg aag ctg ctg aag acg gct gtg ggc 5136
Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
1700 1705 1710

atg cgg gcg ctg ctg gcc acg gtg atg cag gcc ctg ccc cag gtg gag 5184
Met Arg Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly
1715 1720 1725

aac ctg gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gtt ctg 5232
Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
1730 1735 1740

ggc gtg gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt 5280
Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
1745 1750 1755 1760

gag ggc ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc 5328
Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
1765 1770 1775

cta acc ctc ttc cga gtg rcc aca ggt gac aat tgg aat ggc att atg 5376
Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
1780 1785 1790

aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgg tac aac acg 5424
Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
1795 1800 1805

gtc atc acg cct atc ram ttt gtg tcc ttc ghg arg acg gcc cag ttc 5472
Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
1810 1815 1820

grg cta gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag 5520
Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
1825 1830 1835 1840

agc aac aag gag gcc aag gag gag gtc gag ctt gag gct gag ctg gag 5568
Ser Asn Lys Glu Ala Lys Glu Glu Val Glu Leu Glu Ala Glu Leu Glu
1845 1850 1855

ctg gag atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc 5616
Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
1860 1865 1870

ccc ttc ctc tgg cct ggg ctc gag ggc ccc gac agc ccc gac agc acc 5664
Pro Phe Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro
1875 1880 1885

aag cct ggg gct ctg cac cca gag gcc cac gcg aga tca gcc tct cac 5712
Lys Pro Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His
1890 1895 1900

ttt tcc ctg gag cac tcc acg atg cag tcc cac gtc acg gag ctg cca 5760
Phe Ser Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro
1905 1910 1915 1920

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ggg gca gac ttc ctg acc gtg cgg aag tct ggg gtc agc cga agg aac 5808
Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His
            1925                1930                1935

tct ctg ccc aat gac agc tac atg tgt cgg cat ggg agc act gac gag 5856
Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu
        1940                1945                1950

ggg acc ctg gga cac agg ggc tgg ggg ctc ccc aaa gtc aag tca ggc 5904
Gly Pro Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly
    1955                1960                1965

tcc gtc ctg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg 5952
Ser Val Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu
1970                1975                1980

cag ctt ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca 6000
Gln Leu Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro
1985                1990                1995                2000

acc tgg ggc acc atc ccc aaa ctg ccc cca cca gga cgc ccc cct ttg 6048
Thr Trp Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu
                2005                2010                2015

gct cag agg cca ctc agg cgc cag gca gca ata agg act gac tcc tcg 6096
Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu
            2020                2025                2030

gac gtt cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt 6144
Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser
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ggg ccc tcc cag ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca 6192
Gly Pro Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser
    2050                2055                2060

agt acc cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag 6240
Ser Thr Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys
2065                2070                2075                2080

cac atg acc cag cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc 6288
His Met Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly
                2085                2090                2095

aag ggc cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg 6336
Lys Gly Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu
            2100                2105                2110

agc tgg act tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc 6384
Ser Trp Thr Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro
        2115                2120                2125

cca tcc cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc 6432
Pro Ser Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser
    2130                2135                2140

tgt cag cgc cgg ccc acg tcc tgg ttg gat gag cag agg aga cac tcc 6480
Cys Gln Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser
2145                2150                2155                2160

atc gcc gtc agc tgc ctg gat agc ggc tcc caa cct cac ctg gac acg 6528
Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Asp Thr
                2165                2170                2175
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    gac acc tct aac ctc ggg ggc cag cct ctc ggg ggg cct ggg agc cgg   5676
    Asp Thr Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg
                2190                2195                2200

    ccc ccg aaa aaa ggc agg ccg ccc agt gtc acc atg gac gac ccc ccc   6624
    Pro Pro Lys Lys Gly Arg Pro Pro Ser Val Thr Met Asp Asp Pro Pro
            2205                2210                2215

    agc cga ggt cct ggg acc ccg cgc agc ccc ggt atc tgt ctc cgg agg   6672
    Ser Arg Gly Pro Gly Thr Pro Arg Ser Pro Gly Ile Cys Leu Arg Arg
        2220                2225                2230

    agg gct ccg tcc agc gac tct agg gat ccc ttg gcc tct ggc ccc cct   6720
    Arg Ala Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro
    2235                2240                2245

    gac agc atg gct gcc tcg ccc tcc tca aag aaa gat gtg ctg agt ctc   6768
    Asp Ser Met Ala Ala Ser Pro Ser Ser Lys Lys Asp Val Leu Ser Leu
                2250                2255                2260

    tcc ggt tta tcc tct gac cca gca gac ctg gac ccc                   6804
    Ser Gly Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
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  1               5                  10                  15

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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30

ggg ccg ggg tca gga gaa aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttt tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc cgc ccg ggg agc tgg tgt ctc cgc acg gtc tgt aac   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccc tgg ttt gag ggc atc agc atg ttg gtc atc ctc ctc aac tgc gtg   288
Pro Trp Phe Glu Gly Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

acc ctg ggc atg ttc agg cca tgc gag gac atg gcc tgt gac tcc cag   336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
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cgt tgc cgg atc ctg tac gcc ttc gat gac ttc atc ttc gcc aag ttc      384
Arg Cys Arg Ile Leu Tyr Ala Phe Asp Asp Phe Ile Phe Ala Lys Phe
            115                 120                 125

gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttc ggg aag      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
        130                 135                 140

aag ggt tac ctg tgg gac aac tgg aac agg ctt gac ttt ttc atc gtc      480
Lys Gly Tyr Leu Trp Asp Asn Trp Asn Arg Leu Asp Phe Phe Ile Val
    145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tca gct gtc agg acg gtc cgt gtg ctg cga ang ctc agg gcc atc aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

ggg ctg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg ctc ctc agc      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Leu Ser Thr
        195                 200                 205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc      816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cca cgc gag aac ggc atg agg tcc tgc aga agc gtg ccc acg ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc      912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tcc gcg ggg gag cac aac acc ttc aag ggt gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tac gcg tgg atc gcc atc ttc cag gtc acc acg     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac tac gtg atg gat gct cac tcc     1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Tyr Val Met Asp Ala His Ser
        355                 360                 365
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ttc tac aat ttc atc tat ttt att ctc ctc atc ctg ggt ttt tac tgc 1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Val Gly Phe Tyr
    370                 375                 380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag 1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aag cag cgg cgg cag agc cag ctg atg cgg gag cag cgt gtg cgc ttc 1248
Thr Lys Gln Arg Arg Gln Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gac agc acc ctg gct agc ttc tct gag ccc ggc agt tgc 1296
Leu Ser Asn Asp Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gac 1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Asp
        435                 440                 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg 1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
    450                 455                 460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc tag ccc cgc agc agc 1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465                 470                 475                 480

agc tgc tct ngn ncc cac cgc cgc cta tcn gnc cac cac ctg gtg cac 1488
Ser Cys Ser Xaa Pro His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc 1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg 1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tcc cgc cgg ctc arg ctg cca cca ccc tcg acg ccc gcc ctc tca ggg 1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
    530                 535                 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac 1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg ncn cca 1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Xaa Pro
                565                 570                 575

tct gag gca ncn ggc agg act gtg ggc agc ggg aag gtg tat ccc acc 1776
Ser Glu Ala Xaa Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cac acc agc ccc cca ccg gag acg ctg aag gag aag gca ctt gta 1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
        595                 600                 605

gag gtg gct gca agc tat ggg ccc ctt acc ctc acc agc ctc aat atc 1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
    610                 615                 620
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cca ccc ggg ccc tac agc tcc atg cac aag ctg ccc gag ctc gag agc acc gag agt  1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Glu Ser
625                 630                 635                 640

acc ggt gac tgc cca agc tct tgt gag atc tcc agc cct tgt gag aac  1968
Thr Gly Asp Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
                645                 650                 655

gca gac agt gga gcc tgt ggt gcc gac agc tgc ccc tac tgt gcc cgg  2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

ggc ggg gca ggg gag gtg gag ctc gcc gac agt gaa atg cct gac tca  2064
Gly Gly Ala Gly Glu Val Glu Leu Ala Asp Ser Glu Met Pro Asp Ser
        675                 680                 685

gac agc gag gca gtt tat gag ttc acc cag gat gtc cag cac agc agc gac  2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gac ccc cac agc cgg cgg cac cgg agc ctg ggc cca gat gca  2160
Leu Arg Asp Pro His Ser Arg Arg His Arg Ser Leu Gly Pro Asp Ala
705                 710                 715                 720

gag ccc agc tct gtg ccc acc tgg agg ctc atc tgt gac acc ttc  2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                725                 730                 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc  2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
            740                 745                 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc  2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
        755                 760                 765

gag gag ctt acc aac gcc cta gaa atc agt aac atc gtc ttc acc agc  2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    770                 775                 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt  2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785                 790                 795                 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc  2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                805                 810                 815

atc agt gtg tgg gag atc gtg ggc cag cag ggg ggc ggc acg tcg gtg  2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Thr Ser Val
            820                 825                 830

ctg cgg aac ttc cgc ctg ctg agg ctt gtg ctg aag ctg gtg cgc ttc  2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
        835                 840                 845

ccg gcg ctg cag cgg cag ctg gtg gtc atg aag acc atg gac aac  2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    850                 855                 860

gtg gcc acc ttc tgc atg ctg ctc atg ctc ttc atc ttc atc ttc gcc  2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865                 870                 875                 880
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atc ctg ggt atg cac cac ttc ggc tgc aag ccc ggc tac tcg gag cgg gac      2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Pro Ala Ser Glu Arg Asp
                885                 890                 895

ggg gac atc ctg acg gac cgg aag aac ccc gac ttc ttg ctc agg gcc      2736
Gly Asp Ile Leu Thr Asp Arg Lys Asn Pro Asp Phe Leu Leu Arg Ala
            900                 905                 910

atc gtc aac gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc      2784
Ile Val Asn Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
        915                 920                 925

ctc tac aac ggt atg gcc tcc acg ctg ttt tgg gcg gcc atc tat ttc      2832
Leu Tyr Asn Gly Met Ala Ser Thr Leu Phe Trp Ala Ala Ile Tyr Phe
    930                 935                 940

att gcc aac aag acc ttc ggc aac tac gtg cac ttc aat ttg ctg gtc      2880
Ile Ala Asn Lys Thr Phe Gly Asn Tyr Val His Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc      2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tcg gag ccc gat ttc ttt tca ccc agc ctg gat ggt gat ggg gac      2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg      3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                1000                1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac aag gcc gcc gca ccc      3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc      3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc acc agc agc agc agc ggg tcg gca gag cac ggg gcg      3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc      3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac      3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
        1075                1080                1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc tca agt gga gag      3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Ser Ser Gly Glu
    1090                1095                1100

agg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag      3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc ggc cct gcg ggc agt gac cat cgc      3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135
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cac agg ggg act ctg gag cgg gag gcc aag agt tcc ttt gat ctg gca      3984
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150

gac acg ctg cag gtg gca ggg ctg cat cgc aat gcc agt gat gat ggg      4032
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Asp Arg Gly
        1155                1160                1165

tct gtt tct gag tat cag gat tgc aat ggc aag tcg gct tca ggg cgc      4080
Ser Val Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
    1170                1175                1180

ctg gcc cgg gcc ctg cgg tct gat gac ccc cca ctg gat ggg gat gac      4128
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185                1190                1195                1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg      4176
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                1205                1210                1215

atc cga gcc cga ctc cct gcc tgc ctc gag cga gac tcc tgg tca          4224
Ile Arg Ala Arg Leu Pro Ala Cys Leu Glu Arg Asp Ser Trp Ser
            1220                1225                1230

gcc tac atc tcc cct cct cag tgc agg ttc cgc ctc ctg tgc cac ggg      4272
Ala Tyr Ile Ser Pro Pro Gln Cys Arg Phe Arg Leu Leu Cys His Arg
        1235                1240                1245

atc atc acc cac agg ttc gac cac gtg ctc ttt gtc atc atc ttc          4320
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
    1250                1255                1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac      4368
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265                1270                1275                1280

agc gct gaa tgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca      4416
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                1285                1290                1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc      4464
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
            1300                1305                1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg      4512
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
        1315                1320                1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct      4560
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
    1330                1335                1340

gac agc ggc acc aag atc ctg ggc aag ctg agg gtg ctg cgg ctg ctg      4608
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
1345                1350                1355                1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag      4656
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                1365                1370                1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aag ccc atc ggc aac att      4704
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
            1380                1385                1390
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gta gtc atc tgc tgc gcc tcc ctc atc att ttc ggc atc ctg ggc gtg   4224
Val Val Ile Cys Cys Ala Ser Leu Ile Ile Phe Gly Ile Leu Gly Val
        1395                1400                1405

cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggt gag gct acc agg   4272
Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Ala Thr Arg
    1410                1415                1420

aac atc acc aat aaa tcg gat tgt gcc gag gcc agt tac cgg tgg gtc   4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg agg tac ctg   4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                1445                1450                1455

ttc grt ttg gcc tcc aag gat ggt tgg gag gac atc atg tac gat ggg   4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Glu Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc   4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc atc grg gcc ttc ttt   4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt   4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc   4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

cta cga aga ctg gag aaa aag aga agg gaa gcc cag rgc aaa cct tac   4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys Pro Tyr
            1540                1545                1550

tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac tac ttg tgc acc   4704
Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu Cys Thr
        1555                1560                1565

agc cac tag ctg gac ctc ttc atc acm ggt gtn atc ggg ctg aac gtg   4752
Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val
    1570                1575                1580

gtc acc atg gcm arg gag cac tac cag cag ccc cag att ctg gat gag   4800
Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu
1585                1590                1595                1600

gct gtg aag atc tgm aac tac atc ttc act gtc atc ttt gtc ttg gag   4848
Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val Leu Glu
                1605                1610                1615

tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc cag gac   4896
Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp
            1620                1625                1630

agg cgg aac cag ctg gac ctg gcm arn gtg mrg ctg tcc atc ary ggc   4944
Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly
        1635                1640                1645
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atc acg ctg gag gaa atc gag gcc aac gcc tcg ctg ttt atc aat ccc  4992
Ile Thr Leu Glu Glu Ile Glu Ala Asn Ala Ser Leu Phe Ile Asn Pro
    1855                1860                1865

acc atc aat cgc att atg agg gtg ctg cgc att gcc cga gtg ctg aag  5040
Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys
1865                1870                1875                1880

aag gtg aag atg gct gtg ggc atg tgg gcg ctg ctg gac acg gtg atg  5088
Leu Leu Lys Met Ala Val Gly Met Trp Ala Leu Leu Asp Thr Val Met
                1885                1890                1895

cag gcc ctg ccc cag gtg ggg aac ctg gga ttt ctc ttc atg ttg ttg  5136
Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu
            1900                1905                1910

ttt ttc atc ttt gca gct ttg ggc gtg gag ctc ttt ggg gac ctg gag  5184
Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu
        1915                1920                1925

tgt gac gag aca cac ccc tgt gag ggc ttg ggc cgt cac gcc acc ttt  5232
Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe
    1930                1935                1940

cgg aac ttt ggc atg atg ttc ctg acc ctc ttc cga gtc tcc acg ggt  5280
Arg Asn Phe Gly Met Met Phe Leu Thr Leu Phe Arg Val Ser Thr Gly
1945                1950                1955                1960

gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt gac cag  5328
Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln
                1965                1970                1975

gag tcc acc tgc tac aac acg gtg atc tcg cct atc tac ttt gtg tcc  5376
Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser
            1980                1985                1990

ttc gtg ctg acg gcc cag ttc gtg ctg gtc aac gtg gtg atc gcc gtg  5424
Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile Ala Val
        1995                2000                2005

ctg atg aag cac ctg gag gag agc aat aag gag gcc aag gag gag gcc  5472
Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala
    2010                2015                2020

gag ctg gag gct gag ctg gag ctg gag atg agg acc ctc agc ccc cag  5520
Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln
2025                2030                2035                2040

ccc cac tgg cca ctg ggc agc cgc tcc ctc tgg cct ggg gtc gag ggc  5568
Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly
                2045                2050                2055

ccc gac agc aac gac agc ccc aag act ggg gct ctg cac cca gcg gcc  5616
Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro Ala Ala
            2060                2065                2070

cac gcg aga tca gac tcc cac ttt tcc ctg gag cac ccc acg atg cag  5664
His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr Met Gln
        2075                2080                2085

ccc cac ccc acg gag ctg cca gga tcc gac tta ctg act gtg cgg aag  5712
Pro His Pro Thr Glu Leu Pro Gly Ser Asp Leu Leu Thr Val Arg Lys
    2090                2095                2100
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ttt ggg gtc agc cga acg cac tct ctg ccc aat gac agc tcc atg tgt  5760
Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys
1905                1910                1915                1920

cgg cat ggg agc aat gcc gag ggg ccc ctg gga cac aag ggc tgg ggg  5808
Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly Trp Gly
                1925                1930                1935

ctc ccc aaa gct cag tca ggc tcc ghc ttg tcc gtt cac ccc cag cca  5856
Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser Gln Pro
            1940                1945                1950

gca gat acc agc tac atc ctg cag ctt ccc aaa gat gta cat cat ctg  5904
Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro His Leu
        1955                1960                1965

ctc cag ccc cac agc gcc cca act tgg ggc acc atc ccc aaa ctg ccc  5952
Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys Leu Pro
    1970                1975                1980

cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc cag gca  6000
Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala
1985                1990                1995                2000

gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc ggg gaa  6048
Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu
                2005                2010                2015

gac ctg ctg gca gag gtg agt ggg ccc tcc cag ccc ctg gcc cgg gcc  6096
Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala Arg Ala
            2020                2025                2030

tat tct ttc tgg ggc cag tca agt acc cag gca cag cag cac tcc cgc  6144
Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His Ser Arg
        2035                2040                2045

agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct tgc cca  6192
Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro Cys Pro
    2050                2055                2060

ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga agc agt  6240
Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg Ser Ser
2065                2070                2075                2080

tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctt ctg ccc  6288
Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro
                2085                2090                2095

cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag aag tgc  6336
Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys Lys Cys
            2100                2105                2110

tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc tgg ctg  6384
Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser Trp Leu
        2115                2120                2125

gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac agc ggc  6432
Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly
    2130                2135                2140

tcc caa tct cac ctg ggc aca gac ccc tct aac ctt ggg ggc cag cct  6480
Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly Gln Pro
2145                2150                2155                2160
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ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa cct agc aag cct agt  6527
Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser
            2165                2170                2175

atc acc ata gac acc ccc gag agc aag ggt cct cgg act ccg ccc agc  6576
Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro Pro Ser
        2180                2185                2190

cct ggt atc tgc ctc cgg agg agg gat ccg tcc agt gac tcc aag gat  6624
Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser Lys Asp
    2195                2200                2205

ccc ttg gcc tct ggc ccc cct gac agc atg ggt gcc tcg ccc ttc tca  6672
Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro Phe Ser
2210                2215                2220

aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca gca gac  6720
Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Ala Asp
2225                2230                2235                2240

ctg gac ccc                                                     6729
Leu Asp Pro
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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
  1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag   96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg  144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg acg ccg tac ccg gcg cta gcc ccg gtg ggt ttc ttc tac ttg  192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc agc cgc ccg cgg agc tgg tgt acc agc acg gtc tgt aac  240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att gtt gtc aac tgt gtg  288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

act ctg ggt atg ttc agg acg tgt gag gac att gcc tgt gac tcc aag  336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt  384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
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                115                 120                 125

gct gtg gaa atg ggg gtg aag atg gtg gcc ttg ggc att ttc ggg aag   432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aaa tgt tac gtg gga gac ant tgg aac cgg ctt gat tct ttc att gtc   480
Lys Cys Tyr Leu Gly Asp Tar Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc   528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga crg ctc agg gcc att aac   576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac aac ttg   624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg gtc tgt ttc gtc ttc gtc ttt ttc atc   672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc agc aac cgg   720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgn ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag   768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag acn gag aat gag gac gag agc ccc ttc atc tgc tct   816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc acn ctg   864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc   912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat   960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tat gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac   1008
Thr Asn Cys Tyr Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc gca   1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Ala
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gtc atg gac gcc cac ncc   1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aac ttc atc tac ttc att ctc ctc atg atc gtg ggc tcc ttc   1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
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      370                 375                 380
ttc atg atc aac ctg tgc ctg gtg gtg atc gcc acg cag ttc ccc gag  1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Pro Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc  1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat ggt aga acc ctg gca agc ttc tat gag cca ggc agc tgc  1296
Leu Ser Asn Gly Arg Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag ctg aac aag tac ctg gtg tac atc ctc cga aaa gca gcc  1344
Tyr Glu Glu Leu Asn Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg ggt ggg ctg  1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc  1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act ggc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac  1488
Ser Cys Thr Gly Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac cac tac cac ctg ggt aat ggg acg ctc  1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg  1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca gcc tct aca ccc acc ccc tct ggg  1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac  1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca  1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act  1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc act cca cca gag ata ctg aag gat aaa gca cta grg  1824
Val His Thr Ser Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc act agc ttc aac atc  1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
    610                 615                 620

cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt  1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
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625                 630                 635                 640

acg gga gcc tgc gay agc tcc tgc aaa atc ttt agc tct tgc tcc aag 1968
Thr Gly Ala Cys Asp Ser Ser Cys Lys Ile Phe Ser Ser Cys Ser Lys
            645                 650                 655

gca gat agt gga gtc tgc ggg ccg gac agt tgt gcc tam agt gcc cgg 2016
Ala Asp Ser Gly Val Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
        660                 665                 670

aca gga gca gga gag aca gag tcc gct gac cat gtc att tct gac tca 2064
Thr Gly Ala Gly Glu Thr Glu Ser Ala Asp His Val Met Pro Asp Ser
    675                 680                 685

gac agc gag gct gtg tat gag ttt aca cag gac gct cag aac agt gac 2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690                 695                 700

ctc agg gat acc cac agc cgg cga cag cgg agc ctg ggc cca gat 2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atm tgt gac aca 2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
            725                 730                 735

ttc cgg aag atc gta gat agm aaa tac ktt ggc cgg gga atc atg atc 2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
        740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag 2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
    755                 760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc 2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
770                 775                 780

agt ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc 2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg 2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
            805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg 2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Leu Ser
        820                 825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttm 2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
    835                 840                 845

ctg ccg gcc ctg cag cgc cag gtc gtg gtg ctc atg aag acc atg gac 2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc 2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880

agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tat gaa cgg 2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
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                    887                 890                 895

gat ggg gac acg ttg cca gac cgg aag aat ttc gac tac gtg ccc tgt  2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc aat gtc ttt cag att ctg act cag gaa gac tgg aat aaa  2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc cac tac aac ggt atg gcc tcc aca ttg tct tgg gct gct ctt tac  2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg  2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag  2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tcc gag tca gag ccc gat ttc ttt tcg ccc agt gtg gat ggt gat ggg  2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gac cac gcg gaa  3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                 1000                1005

gta cga aag agc cht ttg cca ccc ctc atc atc cat acg gct gcg aca  3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac tcc aag agc tcc agc aca ggt gtg ggg gaa gca ctg  3120
Pro Met Ser His Ser Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt gcc agt agc agt ggg tcc gct gag act gga  3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

ggt gcc cac cat gag atg aaa tgt cag cca agt gcc cgc agc tcc ccg  3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc  3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc  3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg tac cag ctg tct gga gag ggc cag gag agt cag gat  3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac  3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                1125                1130                1135

cat cgc cac agg ggt tcc ttg gaa agt gag gcc aag agt tcc ttt gat  3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
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                1140                1145                1150

ctg cct gac act ctg cag gtg ccg ggg ctg gac ttt aca gcc agc ggc    3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu Asp Phe Thr Ala Ser Gly
        1155                1160                1165

cgg agc tct gcc tct gag aac cag gac tgt aat ggc aag ccg gct tca    3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ala Ala Ser
    1170                1175                1180

ggg cgt ttg gcc cgc aac atg agg act gat gac ccc caa ctg gat ggg    3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                1190                1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgt ata caa    3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                1210                1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc    3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220                1225                1230

tgg tog gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt    3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                1240                1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc    3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
    1250                1255                1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac    3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                1270                1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tac aac tac atc ttc    3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                1290                1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc    3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300                1305                1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg    3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                1320                1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg    4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
    1330                1335                1340

gtc tca gac agc ggg acc aag atc ctt ggc atg ctg agg gtg ctg cgg    4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                1350                1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtg atc agc cgg gcc cag gga    4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                1365                1370                1375

gtg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc    4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380                1385                1390

aac atc gtg gtc act tgt tgt gcc ttc ttc atc att ttt ggc att ctc    4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
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1395                1400                1405

ggg gtg cag gtc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac  4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
1410                1415                1420

atc agg aac atc act aac aaa tct gac tgc gct gag gcc agt tac cga  4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg  4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat  4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc aac atg aac cac  4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
1475                1480                1485

aac ccc tgg atg ctg ctg tac ttc atc tcc ttc ctc ctc atc gtg gcc  4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
1490                1495                1500

ttc ttt gtc ctg aac ctg ttt gtg ggc gtg gtg gag gag gag gtc cat  4560
Phe Phe Val Leu Asn Leu Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag  4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
1525                1530                1535

aag cga ctg cgg agg ctg gag aaa aag aga agg agt gag gag aag cag  4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
1540                1545                1550

atg gcc gaa gcc cag tgc aag ccc tac tac tct gac tac tcg aga ttc  4704
Met Ala Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
1555                1560                1565

cgg ctc ctt gtc cac cac ctg tgt agc agc cac tac ctg gac ctc ttt  4752
Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
1570                1575                1580

atc act ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gaa cat  4800
Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
1585                1590                1595                1600

tac cag cag cct cag atc ctg gac gag gct ctg aag atc tgc aat tac  4848
Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
1605                1610                1615

atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt gtg gac  4896
Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala
1620                1625                1630

ttt ggc ttc cgc cgt ttt ttc cag gac agg tgg aac cag ctg gac ctg  4944
Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
1635                1640                1645

gct att gtg ctt cta tcc atc atg ggc atc aca ctg gag gag att gag  4992
Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu
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      1650                1655                1660

gtc aat ttg tcg ctg ccc att aat ccc acc atc att cgt atc atg agg  5040
Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
1665                1670                1675                1680

gtg ctc tgc att gct cga gtt ctg aag ctg ttg aaq atg gct gtg ggc  5088
Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
                1685                1690                1695

atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag gtg ggg  5136
Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln Val Gly
            1700                1705                1710

aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca gcc ctg  5184
Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
        1715                1720                1725

ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag gca aac aat tgt  5232
Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
    1730                1735                1740

gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg gcc ttt  5280
Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
1745                1750                1755                1760

ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt att atg  5328
Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
                1765                1770                1775

aag gat aac ctc cgg gac tgt gac cag gag tcc acc tgc tat aac act  5376
Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
            1780                1785                1790

gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt  5424
Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
        1795                1800                1805

gtg ctg ctc aac gtg gtc atc gcc gtg ctg atg aag cac ctg gaa gaa  5472
Val Leu Leu Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
    1810                1815                1820

agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag ctg gag  5520
Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu
1825                1830                1835                1840

ctg gag atg aag aag ctc agc aag cag cgc cac tcc ccg ctg ggc agt  5568
Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
                1845                1850                1855

ccc ttc ctc tgg aaa ggg gtg gag ggt gtc aac agt act gac agc cct  5616
Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro
            1860                1865                1870

aag aat ggg gct cca cac acc act gcc cac att gga gca gcc ctg ggc  5664
Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala Ser Gly
        1875                1880                1885

ttg taa ctt gag cac ccc acg atg gta ccc cac ccc gag gag gtg cca  5712
Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu Val Pro
    1890                1895                1900

gtc ccc cta gga cca gac ctg ctg act gtg agg aag tct ggt gtc agc  5760
Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser
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1905                1910                1915                1920

cgg acg cac tct ctg ccc aat gac agc tac atg tgt ggc aat ggg agc   5808
Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser
            1925                1930                1935

act gct gag aga tcc cta ggg cac agg ggc tgg ggg atg cac aaa gcc   5856
Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Met His Lys Ala
        1940                1945                1950

cag tca ggc tcc atc ttg tcc gtt cac tcc caa cta gta gac acc agc   5904
Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Leu Val Asp Thr Ser
    1955                1960                1965

tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg atc cag ccc cat   5952
Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Met Gln Pro His
1970                1975                1980

ggg gct ccc acc tgg ggc gcc atc cct aaa ctc ccc cca cct ggc cgc   6000
Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg
1985                1990                1995                2000

tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata agg act   6048
Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr
                2005                2010                2015

gac tcc ctg gat gtg cag ggc ctg ggt agc cgg gaa gac ctg ttg tca   6096
Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser
            2020                2025                2030

gag gtg agt ggg ccc tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg   6144
Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp
        2035                2040                2045

ggc ggg tcg agc atc cag grg cag cag cgt tcc ggc atc cag agc aaa   6192
Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys
    2050                2055                2060

gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc crg gag ccc   6240
Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro
2065                2070                2075                2080

agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag ctg gac   6288
Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp
                2085                2090                2095

acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc cag gaa   6336
Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu
            2100                2105                2110

gaa ccc ctg ttc cca cgg gac ctg aag aag tgc tac agt gta gag acc   6384
Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr
        2115                2120                2125

cag agc tgc agg cgc agg agt ggg ctc tgg cta gat gaa cag cgg aga   6432
Gln Ser Cys Arg Arg Arg Ser Gly Leu Trp Leu Asp Glu Gln Arg Arg
    2130                2135                2140

ccc tcc att gcc gtc agc tgt ctg gac agc ggc tcc caa ctc cgc cta   6480
His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu
2145                2150                2155                2160

agt cca agc ccc tca agc ctc ggg ggc caa cct ctt ggg ggt cct ggg   6528
Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly
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                2165                2170                2175

agc agg cgt aag aaa aaa ctc agc cca ccc agt atc tct ata gac ccc   6576
Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro
            2180                2185                2190

ccg gag agc cag ggc tct cgg ccc caa tgt agt cct ggt gtc tgc ctc   6624
Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu
        2195                2200                2205

agg agg agg gcg ccg gcc agt gac tct aag gat ccc tcg gtt tcc agc   6672
Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser
    2210                2215                2220

ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac acg ctg   6720
Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu
2225                2230                2235                2240

agt ctc tct ggt ttg tct tct gac cca aca gac atg gac ccc            6762
Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro
                2245                2250
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<210> 6
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atg gac gag gag gag gac gga gcg ggc gcc gag gag tcg gga cag ccc    48
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
 1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag    96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttt tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc cgc ccg cgg agt tgg tgt ctc cgc acg gtc tgt aac   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg   288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

act ctg ggt ang ttc agg ccg tgt gag gac att gcc tgt gaa tta cag   336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt   384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125
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gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag   432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
        130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg att gac ttt ttc att gtc   480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc tcc   528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac   576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg   624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc   672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg   720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc atc ccc gag aac ttc agc ctc atg atg agc gtg gac ctg gag   768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Met Met Ser Val Asp Leu Glu
                245                 250                 255

aat tat tcc cag aca gag aat gag gac gag agc ccc ttc atc tgc tct   816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag ccc cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg   864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

ggt ggg gaa ggt ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc   912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aaa aag tac tat   960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac  1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggg tat gcc tgg atc gcc atc ttc cag gtc atc aca  1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gtc atg gac gct aac aac  1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc  1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380
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ttc acg acc aac ctg tgc ctg gtg gtg att gcc acg cag ttc ccc gag  1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag cag atg agg gag cag cgt gta cga ttc  1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agc acc atg gca agc ttc tct gag cca ggc agc tgc  1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac atg gtg tat atc ctc cga aaa gca gcc  1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg  1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc  1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act agc tca cac cgt cgt ctg tct gcc cac cac ctg gtc cac  1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc  1536
His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtc ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg  1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg  1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac  1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca  1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act  1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg  1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccg agc cct ggg ccc ccc acc cta act ctc acc agc ttc  1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Leu Thr Ser Phe
    610                 615                 620

gca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca acg agt  1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Thr Ser
625                 630                 635                 640
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acg gga gcc tgc cat agt tcc tgc aaa atc tcc agc cct tgc tcc aag                1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac ngt gcc ggg                2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

aca gga gca gga gag cca gag tct gat gac cat gtc atg atc gac aca                2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
        675                 680                 685

gac agc gag gct gtg tat gag ttc acg cag gac gct cag cac agt gac                2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat                2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag atc agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca                2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc                2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
            740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag                2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
        755                 760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc                2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
    770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc                2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg                2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg                2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
            820                 825                 830

gtg ctg cgg acc ttc cgt ctg atg cgg gtg ctg aag ctg gtg cgc ttc                2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
        835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac                2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
    850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc                2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880

agc atc ctg ggc atg cat cnc ttt ggt tgc aag ttc gca tct gaa cgg                2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                885                 890                 895
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gat ggg gac acg ttg cca gac cgg aag aat ttt gat tct gtg ctc tgg   2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
        900                 905                 910

gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa   2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
    915                 920                 925

gcc ctc tac aat ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac   2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aat aag gtg   2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Lys Val
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag   2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg aat ggt gat ggg   2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aaq cgc ttg gcc atg gtg gct ttg gga gaa cac gcg gaa   3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                 1000                1005

cta cga aaq agc att ttg cca ccc ctc atc atc cat acg gct gcg aca   3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac aac aag agc tac agc aca ggt gtg ggg gaa gca ctg   3120
Pro Met Ser His Asn Lys Ser Tyr Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga   3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tca cag   3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc   3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc   3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat   3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa agg gac cgg gcc agc cca gca ggc agt gac   3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                1125                1130                1135

cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ctt gac   3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
            1140                1145                1150
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ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc  3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
        1155                1160                1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca  3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
    1170                1175                1180

ggg cgt ttg gca cgc acc ctg agg act gat gac ccc caa ctg gat ggg  3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                1190                1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa  3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                1210                1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc  3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220                1225                1230

tgg tcg gcc tat atc ttt ccc cct cag tca agg ttt cgt ctc ctg tgt  3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                1240                1245

cac cgg atc atc aac cac aag atg ttt gac cat gtg gtc ctc ghc atc  3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
    1250                1255                1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac  3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                1270                1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc  3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                1290                1295

acg gca gtc ttt cta gct gaa atg ana gtg aag gtg gtg gca ctg ggc  3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300                1305                1310

tgg tgc ttt ggg gag cag gnc nac ctg cgc agc agc tgg aat gtg ctg  3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                1320                1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg  4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
    1330                1335                1340

gtc tcc gac agc ggc acc aag atc ttt ggc atg ctg agg gtg ctg cgg  4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                1350                1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga  4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                1365                1370                1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc  4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380                1385                1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att gtc  4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Val
        1395                1400                1405
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ggg gtg cag ccc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac  4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
      1410                1415                1420

aac agg aac atc act aac aaa tcc gac tgc gct gag gac agt tac cga  4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
  1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac atg ggt cag gct ctg atg  4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat  4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
            1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac  4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
        1475                1480                1485

aac ccc tgg atg ctg gta tac ttc atc tcc ttc ctc ctc atc gtg gcc  4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
    1490                1495                1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat  4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag  4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga ctg cgg agg ctg gag aaa aag aga agg aat ctg atg ttg gac  4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp
            1540                1545                1550

gat gta att gct tcc ggc agt tca gcc agc gct gcg tca gaa gcc cag  4704
Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln
        1555                1560                1565

tgc aag ccc tac tac tct gac tag tog aga ttc cgg atg gtt gtc cac  4752
Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His
    1570                1575                1580

cac ctg tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc  4800
His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile
1585                1590                1595                1600

ggg ctg aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag  4848
Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln
                1605                1610                1615

atc ctg gac gag gct ctg aag atc tgc aat tac atg ttt acc gtc atc  4896
Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile
            1620                1625                1630

ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt  4944
Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg
        1635                1640                1645

ttc ttc cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg  4992
Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu
    1650                1655                1660
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tcc att atg ggc atc acc ctg gag gag att gag gtc aac ctg tcg ctg  5043
Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu
1665                1670                1675                1680

ccc atc aac ccc acc atc atc cgt atc atg agg gtg ctc ggc att gct  5088
Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala
                1685                1690                1695

cga gtt ctg aag ctg ttg aag atg gtt gtg ggc atg cgg gca ctg ctg  5136
Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu
            1700                1705                1710

cac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctt  5184
His Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu
        1715                1720                1725

ttc atg tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt  5232
Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe
    1730                1735                1740

gga gac ctg gag tgt gat gag aca cac cct tgt gag ggc tcg ggt cgg  5280
Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg
1745                1750                1755                1760

cat gcc acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga  5328
His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg
                1765                1770                1775

gtc tcc act ggt gac aac tgg aat ggt att atg aag gac acc tcc cgg  5376
Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg
            1780                1785                1790

gac tgt gac cag gag tcc acc tgt tac aac act gtc atc tcc cct att  5424
Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile
        1795                1800                1805

tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg  5472
Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val
    1810                1815                1820

gtc ata gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc  5520
Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala
1825                1830                1835                1840

aag gag gag gcc gag ctc gag gcc gag ctg gag ctg gag atg aag acg  5568
Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr
                1845                1850                1855

ctc agc ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc  5616
Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro
            1860                1865                1870

ggg gtg gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca  5664
Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro
        1875                1880                1885

cat aac act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac  5712
His Thr Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His
    1890                1895                1900

ccc acg atg gta ccc cac ccc gag gag gtg cca gtc ccc cta gga cca  5760
Pro Thr Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro
1905                1910                1915                1920
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gat ctg ctg act gtg agg aag tcc ggt gtc agc cgg acg cac tct ctg   5808
Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
            1925                1930                1935

cct aat gac agc tac acg tgc cgc aat ggg agc act gct gag aga tcc   5856
Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser
        1940                1945                1950

cta gga cac agg ggc tgg ggg ctt ccc aaa gac cag tca ggc tcc atc   5904
Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile
    1955                1960                1965

ttg tcc gtt cac tcc caa cca gca gac acc agc tgc atc cta cag ctt   5952
Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu
1970                1975                1980

ccc aaa gat gtg cac tat ctg ctc cag cct cat ggg gcc ccc acc tgg   6000
Pro Lys Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp
1985                1990                1995                2000

ggc gcc atc cct aaa cta ccc cca cct ggc cgc tcc cct ctg gct cag   6048
Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
                2005                2010                2015

agg aat ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg   6096
Arg Asn Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
            2020                2025                2030

cag ggc ctg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc   6144
Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro
        2035                2040                2045

tca tgc cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg tcg agc atn   6192
Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile
    2050                2055                2060

cag gtg aag cag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc   6240
Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile
2065                2070                2075                2080

cgc ctg tca gcc cct tgc cca ggc ctg gaa ccc agc tgg gcn aag gac   6288
Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp
                2085                2090                2095

cct cna gag acc aga agt agc tta gag ctg gac acg gag ctg agc tgg   6336
Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
            2100                2105                2110

att tca gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttc cca   6384
Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro
        2115                2120                2125

cgg gac ctg aag aag tgc tac agt gtg gag acc cag agc tgc agg cgc   6432
Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg
    2130                2135                2140

agg cct ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gat gtc   6480
Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Asp Val
2145                2150                2155                2160

agc tgt ctg gac agc ggc tcc daa ccc cgc cta tgt tca agn nnn tca   6528
Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser
                2165                2170                2175
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agc ctc ggg ggt caa cct ctt ggg ggt cct ggg agc cgg cac aag aaa  6576
Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys
        2180                2185                2190

aaa ctc agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc  6624
Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly
    2195                2200                2205

tct cgg ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg  6672
Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro
2210                2215                2220

gcc agt gac tct aag gat ccc tcg gtc tcc agc ccc ttt gac agc acg  6720
Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr
2225                2230                2235                2240

gct gcc tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg  6768
Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu
                2245                2250                2255

tct tct gac cca aca gac atg gac ccc                             6795
Ser Ser Asp Pro Thr Asp Met Asp Pro
            2260                2265
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<210> 7
<211> 6816
<212> DNA
<213> Rattus sp.

<220>
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<400> 7

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atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc   48
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
  1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag   96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg  144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg  192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac  240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc ctc aac tgt gtg  288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Leu Asn Cys Val
                85                  90                  95

acc ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag  336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
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cgc tgc cgg atc ctg cag gcc ttc gat gac tac atc ccc gcc ttt ttt   384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Pro Ala Phe Phe
            115                 120                 125

gct gtg gag atg gtg gtg aag atg gtg gcc ttg ggt atc ttt ggg aag   432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
        130                 135                 140

aaa tgt tac ctg ggg gac act tgg aac cgg ctt gac ttt ttc att gtc   480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggt atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc   528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cag cag ctc agg gcc att aac   576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctg gtc aca tta ctg ctg tac gac acc   624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Tyr Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc   672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgg aac cgg   720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ccc gat gag aac tcc agc ctc ccc ctg agc gtg gac ctg gag   768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct   816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg   864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc   912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat   960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct ggg ggt gag cac aac ccc ttc aaa ggc gcc atc aac  1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca  1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc  1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365
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ttc tac aac ttc atc tat ttc atc ctt ctc acc atc gtg ggg tcc ttc 1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
        370                 375                 380

ttc atg atc aac atg tgc ctg gtg gtg att gcc acg cag ttc tcc gag 1200
Phe Met Ile Asn Met Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc 1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agt aac ctg gca agc ttc tct gag gca ggc agc tgc 1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Trp Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac ctg tac atc ctc cga aaa gca gcc 1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg 1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc 1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgt act cgc tca cac cgt cgt ctg tct gtc cac cac crg gtc cac 1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cat ctg ggt aat ggg acg ctc 1536
His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg 1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc agg ctc atg cta cca aca acc tct aca ccc act ccn tat ggg 1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac 1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct cnc aga tgc cca 1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act grg ggt agt ggg aag gtg tan ccc act 1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg 1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ttc acg agc ttc aac atc 1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
    610                 615                 620
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tcc cct ggg ccc ttc agt ccc atg cac aag ctc ctg gag acc cag agt  1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

agg gga gcc tgc cat agt ccc tgc aaa atc tcc agc ccc tgt tcc aag  1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tat tgt gcc cgg  2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

aca gga gca gga gag ccc gag tcc gct gac cat gtc atg cct gac tca  2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
        675                 680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac  2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

cgc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat  2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca  2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc  2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
            740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag  2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
        755                 760                 765

ccc gag gag ctt acc aac gcc ctg gaa atc agc aac atc gtc ttc aac  2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
    770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc  2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg  2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg  2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Leu Ser
            820                 825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc  2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
        835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac  2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
    850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc  2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880
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agc atc ctg ggc aag cat ctc ttt ggt tgc aag ttc gca tct gaa cgg  2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
            885                 890                 895

gat ggg gac acg ttg cca gac cgg aag aat ttt gac tcc ctg ctc tgg  2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
        900                 905                 910

gcc atc gtc act gtt ttt cag att ctg act aag gaa gac tgg aat aaa  2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
    915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gat gct ctt tac  2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Asp Ala Leu Tyr
930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg  2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

ggg gcc att ctt gcg gaa gga ttt cag gca gag gga gat gcc acc aag  2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gac ggg  2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa  3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Gln
        995                 1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca  3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg  3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga  3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc tgc agc tcc ccg  3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc  3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agt  3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc aag gag agt cag gat  3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc aca gaa ggc agt gac  3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                1125                1130                1135
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cat tgt cac agg ggt tcc ttg gaa agt gag gcc aag agt ttc ttt gat  3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
        1140                1145                1150

ctg tct gac acc ctg cag gtg ccg ggg ctg cac cgc ahc ycc agc ggc  3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
    1155                1160                1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggt aag tcg gct tca  3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
1170                1175                1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg  3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                1190                1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa  3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                1210                1215

gct tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc  3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220                1225                1230

tgg tcg gac tat atc ttt cct gct cag tma agg ttt cgt ctc ctg tgt  3744
Trp Ser Asp Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                1240                1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc  3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
    1250                1255                1260

atc ttm ctc aac tgt atc acc atc gch atg gag cgc ccc aaa att gac  3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                1270                1275                1280

ccc cac agc gct gag cgc atc ttc ctg acm atc tmm aac tac atc ttc  3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                1290                1295

acg gca gtc ttt cts gnt gaa atg aca gtg aag gtg gtg gca ctg ggc  3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300                1305                1310

tgg tgc ttt ggg gag cag gac tac ctg cgc agc agc tgg aat gtg ctg  3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                1320                1325

gac ggc ttg atg gtg ctc atc tcc gtc atc gac ata ctg gtc tcc atg  4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
    1330                1335                1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg  4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                1350                1355                1360

ctg ctg cgg acc ctg cgt tca ctc agg gtc atc agc cgg gam cag gga  4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Glu Gly
                1365                1370                1375

ctg aag atg gtg gta gag act ctg atg tca tcc ctc aaa tcc att ggc  4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380                1385                1390
```

aac att gtg gtc att tgc tgt gcc ttc ttc atc att tcc gga atc ctc 4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
1395 1400 1405

ggg gtg cag ctc ttc aaa ggg aag ttc ttt gtg tgt cag ggt gag gac 4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
1410 1415 1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agt tac cga 4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425 1430 1435 1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg gcc cag gct ctg atg 4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
1445 1450 1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat 4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
1460 1465 1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac 4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
1475 1480 1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc 4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
1490 1495 1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat 4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505 1510 1515 1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag 4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
1525 1530 1535

aag tga cta cgg agg ctg gag aaa aag aga agg agt aag gag cag cag 4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
1540 1545 1550

atg gcc gat cta atg ttg gac gat gta att gct tcc ggc agt tca gcc 4704
Met Ala Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala
1555 1560 1565

agc gct gtg tca gaa gcc cag tgc aag ccc tac tac tct gac tac tcg 4752
Ser Ala Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser
1570 1575 1580

aga ttc cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac 4800
Arg Phe Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp
1585 1590 1595 1600

ctc ttc atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg 4848
Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met
1605 1610 1615

gaa cat tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc 4896
Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys
1620 1625 1630

aat tac atc ttt acc gtc atc ttt gcc ttt gag tca gtt ttc aag ctc 4944
Asn Tyr Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu
1635 1640 1645

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gtg gcc ttt ggc ttc ggt ggt ttc ttc aag gat agg tgg aac gag ctg  4992
Val Ala Phe Gly Phe Gly Arg Arg Phe Phe Gln Asp Arg Trp Asn Glu Leu
     1650                1655                1660

gac ctg gct att gtg ctt ctg tcc atc atg ggc atc aca gtg gag gag  5040
Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu
1665                1670                1675                1680

act gag gtc aat ctg tcg ctg ccc atc aac ccc acc atc atc cgt atc  5088
Ile Glu Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile
                1685                1690                1695

atg agg gtg ctc cgc att gct gga gtt ctg aag ctg ttg aag atg gct  5136
Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala
            1700                1705                1710

gtg ggc atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag  5184
Val Gly Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln
        1715                1720                1725

gtg ggg aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca  5232
Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala
    1730                1735                1740

gct ctg ggn gtg gag ctc ttt gga gac ctg gag tgt gat gag tca cac  5280
Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His
1745                1750                1755                1760

cct tgt gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg  5328
Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met
                1765                1770                1775

gcc ttt ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt  5376
Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly
            1780                1785                1790

att atg aag gac acc nnn ngg gac tgt gac cag gag tcc acc tgc tac  5424
Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr
        1795                1800                1805

aac ant gtc atc tcc cct atc tac ttt gtg tcc ttc ghg ctg acg gcc  5472
Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala
    1810                1815                1820

cag ttt gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg  5520
Gln Phe Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu
1825                1830                1835                1840

gaa gaa agc aac aaa gay gcc aag gag gag gcc gag ctc gag gcc gag  5568
Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu
                1845                1850                1855

ctg gag ctg gag atg aag acg ctt agc nng cag ccc cac tcc ccy ctg  5616
Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu
            1860                1865                1870

ggc agc cdc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac  5664
Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp
        1875                1880                1885

agt cct aag cct ggg gat bha cac acc act gcc cac att gga gca gcc  5712
Ser Pro Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala
    1890                1895                1900
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tcg ggc ttt tcc cct gag cct ttt acg atg gta ttt cct gag gag 5760
Ser Gly Phe Ser Leu Glu His Phe Thr Met Val Phe Pro Glu Glu
1905                1910                1915                1920

gtg tca gtc ccc ctg ggc tcc gat gtg gtt ctg atg ttg agg aag tct ggt 5808
Val Pro Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly
                1925                1930                1935

gtc ggc cgg acg cac tct ctg ccc aat gac agc tac atg tgc cgc aat 5856
Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn
        1940                1945                1950

ggg agc act gct gag aga tcc ctg gga cac agg ggc tgg ggg ctc ccc 5904
Gly Ser Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro
    1955                1960                1965

aaa gac cag tca ggc tcc atc tgg tcc gtt cac tcc caa cca gca gac 5952
Lys Ala Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp
1970                1975                1980

acc agc tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg ctc cag 6000
Thr Ser Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln
1985                1990                1995                2000

ccc cat ggg gct ccc acc tgg ggc gcc atc cct aaa ctg ccc cca cct 6048
Pro His Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro
                2005                2010                2015

ggc agc tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata 6096
Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile
            2020                2025                2030

agg act gac tcc ctg gat gtg cag ggc ctg ggt agc ggg gaa gac ctg 6144
Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu
        2035                2040                2045

ttg tca gag gtg agt ggg ccc tcc tgc cct ctg acc tgg tcc tca tcc 6192
Leu Ser Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser
    2050                2055                2060

ttc tgg ggc ggg tcg agc atc cag gtg cag cag cgt tcc ggc atc cag 6240
Phe Trp Gly Gly Ser Ser Ile Glu Val Gln Gln Arg Ser Gly Ile Gln
2065                2070                2075                2080

agc aaa gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg 6288
Ser Lys Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu
                2085                2090                2095

gaa ccc agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag 6336
Glu Pro Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu
            2100                2105                2110

ctg gac acg gag ctg agc tgg att tca gga gac ctc ctt ccc agg agc 6384
Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser
        2115                2120                2125

cag gaa caa ccc ctg ttc cca agg gac ctg aag aag tgc tac agt gta 6432
Gln Glu Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val
    2130                2135                2140

gag acc cag agt tgc agg cgc agg cct ggg ttc tgg tta gat gaa cag 6480
Glu Thr Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln
2145                2150                2155                2160
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cgg aga cac aac ttt gtt gcc agc tgt ctg gac agc ggc tcc caa acc   6528
Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Thr
                2165                2170                2175

cgc cta tgt cca agc ccc tcc agc ctc ggg ggc cac cct cat ggg ggt   6576
Arg Leu Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly
            2180                2185                2190

cct ggg agc cgg cct aag aaa aaa ctc agc cca ccc agt atc tct atn   6624
Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile
        2195                2200                2205

gac ccc ccg gag agc aag ggc tct cgg ccc cca tgg agt cct ggt gtc   6672
Asp Pro Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val
    2210                2215                2220

tgc ctc agg agg agg gcg acg gcc agt gac tct aag gat cca tcg gtc   6720
Cys Leu Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val
2225                2230                2235                2240

tcy agc ccc ctt gac agc acg gct gmc tna ccc tcc cca aag aaa gac   6768
Ser Ser Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp
                2245                2250                2255

acg ctg agt ctn tct ggt ttg tct tct gac cca aca gac atg gac ccc   6816
Thr Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro
            2260                2265                2270


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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
  1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag   96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg acg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg cta gcc cog gtg gtt ttc ttc tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc agc cgc ccg cgg agc tgg tgt ctc ggc acg gtc tgt aac   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac ggt gtg   288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

act ctg ggt atg tac agg acg tgt gag gac att gcc tgt gac tta cag   336
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Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asn Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gac ttc ttt  384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc act ttt ggg aag  432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc  480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc  528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cgc ccg ctc agg gcc att aac  576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att gtc gcc aca ttg ctg ctg gac acc ttg  624
Arg Val Pro Ser Met Arg Ile Val Ala Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc  672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc ttg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg  720
Phe Gly Ile Leu Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttt ctc ccc gag aac ttc agc ctg ccc ctg agc ttg ctg gac ctg  768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tcc  816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg  864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc  912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtt aac tgg aac cag tac tat  960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gag ggc gag cac aac ccc ttc aaa ggc gcc atc aac 1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg 1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac tac gta atg gac gct cac tcc 1104
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Leu Gln Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        350                 360                 365

ttc tac aac ttc atc tac tcc atc ctc gtc atc atc gtg ggc tcc ttc  1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380

tcc agg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag  1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg agg cgg gag cag cgt gta cga ttc  1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag ccc ggc agc tgc  1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag ctg ctc aag tac ctg gtg tac atc gtc cga aaa gca gcc  1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gac cag gtc tct agg gct atg ggc gtg cgg gct ggg ctg  1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc  1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act agc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac  1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ccc  1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

agg gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg  1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc tgg atc acg cta cca ccg ccc tct acg ccc act ccc tct ggg  1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac  1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca grc cgt tgc cag gca ccc cct ccc agg tgt ccc  1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act  1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agt cct cca cca gag ata ctg aag gat aaa gca tta gtg  1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc act ggg ccc acc acc ctc acc agc agc ttc aac  1872
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Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
        610                 615                 620

gca cct ggg gct ttc agc tcc atg cac aag ctc ctg gag aca cag agt                1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

acg ggc gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag                1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg                2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

aca gga gca gga gag cca gag tcc gct gac cat gcc atg cct gac tca                2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
        675                 680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac                2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat                2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag ctt agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca                2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc                2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
            740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggt atc gag tac cac gag cag                2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
        755                 760                 765

ccc gag gag atg aac aac gcc ctg gag atc agc aac atc gtc ttc acc                2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
    770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctt gtc tac ggt gcc                    2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg                2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg                2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
            820                 825                 830

gtg ctg cgg acc ttc cgc ctg ctg cgg gtg ctg aag ctg gtg cgc ttc                2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
        835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac                2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
    850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ttc atg ctg ttc atc ttc agc ctc                2640
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Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880

agt atc ctg ggc atg cac ctc ttt ggt tgc aag ttc gca tct gaa cgg                2689
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                885                 890                 895

gat ggg gac acg ttg gca gac cgg aag aat ttc gat tcc ctg ctc tgg                2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc act gtc ttt cag att ctg aat cag gaa gac tgg aat aaa                2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gat gtt tac                2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Asp Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg                2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att att gtg gaa gga ttc cag gca gag aga gat gcc acc aag                2928
Val Ala Ile Ile Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tat gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg                2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gag                3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                 1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gat gcg acc                3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg                3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga                3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

gat gcc cac car gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg                3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc                3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc                3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg ccc ctg ctg tct ggc gag ggc cag gag agt cag gat                3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac                3408
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Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
            1125                1130                1135

gat cgc cac agg ggt tcc ctg gaa cgt gag gcc aag agt tac ctt gac    3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Tyr Phe Asp
        1140                1145                1150

ctg cct gac act ctg cag gtg cag ggg ctg cac cgc atg gcc agc ggc    3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
    1155                1160                1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gcc tca    3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
1170                1175                1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg    3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                1190                1195                1200

gat gat gac aat gat gag ggc aat ctg agc aaa ggg gaa cgc ata cag    3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                1210                1215

gcc tgg gtc aga tcc cgg ttt cct gcc tgt tgc cga gag cga gat tcc    3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220                1225                1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt    3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                1240                1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc    3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
    1250                1255                1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc cac aaa att gac    3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                1270                1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc    3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                1290                1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc    3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300                1305                1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg    3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                1320                1325

gac ggc ttg ctg gtg gtc atc tcc gtc atc gac atc ctg gtc tcc atg    4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
    1330                1335                1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg    4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                1350                1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc tgg gcc cag gga    4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                1365                1370                1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aag ccc att ggc    4176
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Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
        1380                1385                1390

aac att gag gtc att tgc tgt gcc ttc atc att ttg ggc att ctc      4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
    1395                1400                1405

ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag gct gag gac   4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
1410                1415                1420

acc agg aac atc act ser aaa tcc gac tgc gct gag gcc agc tac cga   4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425                1430                1435                1440

tgg gtc cag cac aag ttc aac ttt gac aac ctg ggc cag gct ctg atg   4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gtc tcc aag gat ggt tgg gtt gac atc atg tat   4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
            1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac aac   4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn Asn
        1475                1480                1485

aac ccc tgg atg ctg ctc tac ttc atc tcc ttc ctc ctc atc gtg gcc   4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
    1490                1495                1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat   4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag   4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga ctg agg agg ctg gag aaa aag aga agg aaa gcc cag tgc aag   4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys
            1540                1545                1550

ccc tac tac tct gac tac tcg agg ttc cgg ctc ctt gtc cac cac ctg   4704
Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
        1555                1560                1565

tgt acc agc cac tac ctg gac ctg ttc atc act ggt gtc atc ggg ctg   4752
Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
    1570                1575                1580

aac gtg gtc acc atg gcc atg gaa cat tac cag cag ccc cag atc ctg   4800
Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
1585                1590                1595                1600

gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc ttt gtc   4848
Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
                1605                1610                1615

ttt gag tca gtt ttc aaa ctt ctg gcc ttt ggc tac cyc ggt ttc ttc   4896
Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
            1620                1625                1630

cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg tcc mtc   4944
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Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
        1635                1640                1645

gtg ggc atc acg ctg gag gag att gag gtc aac ctg tcg ctg ccc atc  4992
Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu Pro Ile
    1650                1655                1660

aac ccc acc atc atc agt atg acg gtg ctc ggc atc gcc gcg gtt      5040
Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val
1665                1670                1675                1680

ctg aag ctg ttg aag atg gct gtg ggc atg cgg gcg ctg cac acg      5088
Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu His Thr
                1685                1690                1695

gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg  5136
Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met
            1700                1705                1710

tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac  5184
Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp
        1715                1720                1725

ctg gag tgt gat gag aca cac ccc tgt gag ggc ttg ggt cgg cat gcc  5232
Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
    1730                1735                1740

acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga gtc tcc  5280
Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser
1745                1750                1755                1760

act ggt gac aac tgg aat ggt att atg aag gac acc ctc cgg gac tgt  5328
Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys
                1765                1770                1775

gac cag gag tcc acc tgc tac aac act gtc atc tcc cct atc tac ttt  5376
Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
            1780                1785                1790

gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg gtc ata  5424
Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
        1795                1800                1805

gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc aag gag  5472
Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
    1810                1815                1820

gag gcc cag ctc gag gcc gag atg gag ctg gag atg aag acg ctc agc  5520
Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
1825                1830                1835                1840

ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc ggg gtg  5568
Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
                1845                1850                1855

gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca cac acc  5616
Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro His Thr
            1860                1865                1870

act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac ccc acg  5664
Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His Pro Thr
        1875                1880                1885

atg gta ccc cac ccc gag gag gtg cca gtt ccc cta ggg ccc gac ctg  5712
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Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro Asp Leu
1890                1895                1900

ctg acc gtg agg aag tat ggt gtc agc agg acg cac tct ctg ccc aat                5760
Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn
1905                1910                1915                1920

gac agc tac atg tgt cgc aat ggg agc act gcc gag aga tcc cta gga                5808
Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser Leu Gly
                1925                1930                1935

cac agg ggc tgg ggg ctc ccc aca gtc cag tca ggc tcc atc ttg tcc                5856
His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile Leu Ser
        1940                1945                1950

gtt cac tcc caa ccA gca gac acc agc tgc atc cta cag ctt ccc aaa                5904
Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu Pro Lys
    1955                1960                1965

gat gtg cac tat ctg ctc cag cct cat ggg gct ccc acc tgg ggc gcc                5952
Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp Gly Ala
1970                1975                1980

atc cct aaa cta ccc cca gct ggc cgc tcc cct ctg gct cag agg cct                6000
Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro
1985                1990                1995                2000

ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg cag ggc                6048
Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly
                2005                2010                2015

atg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc tcc tgc                6096
Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro Ser Cys
            2020                2025                2030

cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg teg agc atc cag gtg                6144
Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile Gln Val
        2035                2040                2045

cag gag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc agt ctg                6192
Gln Glu Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile Arg Leu
    2050                2055                2060

cca gcc ccA kgc cca ggc ctg gaa ccc agc tgg gcc aag gac cct cca                6240
Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp Pro Pro
2065                2070                2075                2080

gag acc aga agc agc tta gag ctg gac arg gag ctg agc tgg att tca                6288
Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser
                2085                2090                2095

gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttt cca cgg gac                6336
Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro Arg Asp
            2100                2105                2110

ctg aag aag tgc tac agt gta gag acc cag agc tgc agg cgc agg cct                6384
Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg Arg Pro
        2115                2120                2125

ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gct gtc agc tgt                6432
Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys
    2130                2135                2140

ctg gac agc ggc tcc caa acc cgc cta tgt cca agc acc tca agc ctc                6480
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Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Arg Ser Ser Leu
2145                2150                2155                2160

ggg ggc caa ccc ctt ggg ggt ccn ggg agc cgg cct aag aaa aaa ctt      6528
Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu
                2165                2170                2175

agc cca ccc agt arg ccc ata gac ccn ccg gag agc cag ggg tct cgg      6576
Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly Ser Arg
            2180                2185                2190

ccc cca tgc agt ccc ggt gtc tgt cnn agg agg agg gcg ccg gcc agt      6624
Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro Ala Ser
        2195                2200                2205

gac tct aag gat ccc tcg gtc tcc agc ccc ctt gac agc acg gct gcc      6672
Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr Ala Ala
    2210                2215                2220

tca ccc tnc cca agg aaa gac acg ctg agt ctc tct ggt ttg tct nct      6720
Ser Pro Ser Pro Arg Lys Asp Thr Leu Ser Leu Ser Gly Leu Ser Ser
2225                2230                2235                2240

gac cca acn gac atg gac ccc                                         6741
Asp Pro Thr Asp Met Asp Pro
                2245


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Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly
  1               5                  10                  15

agc agc ccc tgg ccc ngn ggg gtt ggt ggg ggc gtc ccc gga gag ccc      96
Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
            20                  25                  30

cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca     144
Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
        35                  40                  45

ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac     192
Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
    50                  55                  60

gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc     240
Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
65                  70                  75                  80

tgc atn ggt cag agc acg cgg cag cgc agc tgg tgc ctc cgg ctg gtc     288
Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
                85                  90                  95

tgc aac cna tgg ttc gag cac gcg agc atg ctg gta atc atg ctc aac     336
Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn
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                100                 105                 110

tgc gtg acc ctg ggc atg ttc ggg ccc tgt gag gac gtt gag tgc ggc  384
Cys Val Thr Leu Gly Met Phe Gly Pro Cys Glu Asp Val Glu Cys Gly
    115                 120                 125

tcc gag ggc tgc aac atc ctg gag gcc ttt gac gcc ttc ark ttc gcc  432
Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
130                 135                 140

ttt ttt gcg gtg gag atg gcc atc aag atg gtg gac rkg ggg ctg ttc  480
Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
145                 150                 155                 160

ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc  528
Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
                165                 170                 175

atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg  576
Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
            180                 185                 190

agc ctc tmg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc  624
Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
        195                 200                 205

atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat  672
Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
    210                 215                 220

acg ctg ccc atg ctc ggg aac gtc ctt ctg ctg tgc ttc ttc gtc ttc  720
Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
225                 230                 235                 240

ttt att ttc ggg atm gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg  768
Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                245                 250                 255

aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc  816
Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
            260                 265                 270

ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc  864
Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
        275                 280                 285

atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc  912
Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
    290                 295                 300

ccc ggc cgc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc  960
Pro Gly Arg Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
305                 310                 315                 320

tac acg cag ccg cag gcc gag ggg gtg ggc gct gca ggc aac gcc tgc  1008
Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
                325                 330                 335

atc aac tgg aac cag tac tac aac gtg tgc cgc tcg ggc gac tcc aac  1056
Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
            340                 345                 350

ccc cac aac ggt gcc atc aac ttc gac aac acc tgc tac gcc tgg att  1104
Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
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                355                 360                 365

gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac att atg cac  1152
Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met His
    370                 375                 380

tac gtc atg gac gcc cac tta ttt tac aac ttc atc tat ttt atc ctg  1200
Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
385                 390                 395                 400

ctc atc atc gtg ggc tcc ttc ttt atg atc aac ctg tgc atg gtg gtg  1248
Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Met Val Val
                405                 410                 415

att gtc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg  1296
Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
            420                 425                 430

cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc  1344
Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
        435                 440                 445

ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc  1392
Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
    450                 455                 460

cac atc ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gac cgc  1440
His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
465                 470                 475                 480

tgg cag agc cgc tgg cgc aag aag gtg gac cac agt gct gtg cca ggc  1488
Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                485                 490                 495

cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg  1536
Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
            500                 505                 510

gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac  1584
Val His His Leu Val Tyr His His His His His His His His His Tyr
        515                 520                 525

cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc  1632
His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
    530                 535                 540

tgc gac acc agg ctg gtc cga gct cgc gcg ccc ccc tcg cca cct tcc  1680
Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
545                 550                 555                 560

cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat  1728
Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                565                 570                 575

gcc gac tgc cac ata gag ggg ccg cag gag agg gcc agg gtg ggc acc  1776
Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
            580                 585                 590

tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg  1824
Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
        595                 600                 605

cac cat gaa gta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa  1872
His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
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      610                 615                 620

     agg gag cac cag ccc cgg acc cag ggg gaa gtg ggc cgg tgg acc gtc      1920
Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Val
625                 630                 635                 640

     agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc ccc gac ccc tac      1968
Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
                    645                 650                 655

     gag aag atc ccg cac gtg gcc ggg gag cag gga ctg ggc cag gcc gct      2016
Glu Lys Ile Pro His Val Ala Gly Glu Gln Gly Leu Gly Gln Ala Pro
                660                 665                 670

     ggc cat ctg tcg ggc ttc agt gtg ccc tgc ccc ctg ccc agc ccc cca      2064
Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
            675                 680                 685

     gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt      2112
Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
        690                 695                 700

     gcc ctg gag gac ccg gag ggt gag ttc agc ggc tcg gaa agt gga gac      2160
Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
705                 710                 715                 720

     tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt      2208
Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                725                 730                 735

     gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc      2256
Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
            740                 745                 750

     cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc cag      2304
Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
        755                 760                 765

     ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag      2352
Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
    770                 775                 780

     ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg      2400
Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
785                 790                 795                 800

     gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag      2448
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                805                 810                 815

     ccc gag gag ctg act aat gat ctg gag atc agc aac atc gtg ttc acc      2496
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
            820                 825                 830

     agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct      2544
Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
        835                 840                 845

     ctg ggc tac atc cgg aac ccg tac aac atc ttt gac ggc atc atc gtg      2592
Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
    850                 855                 860

     gtc atc agc gtc tgg gag atc gca ggg cag gcg gac ggt ggc ttg tct      2640
Val Ile Ser Val Trp Glu Ile Ala Gly Gln Ala Asp Gly Gly Leu Ser
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      865                 870                 875                 880

gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttc   2688
Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
                885                 890                 895

ctg cca gcc ctg cgg cgc cag ctc gtg gtg atg atg aag acc atg gac   2736
Leu Pro Ala Leu Arg Arg Gln Leu Val Val Met Met Lys Thr Met Asp
            900                 905                 910

aac gtg gct acc ttc tgc atg ctg ctc atg atc ttc atc ttc atc ttc   2784
Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
        915                 920                 925

agc atc ctg ggc atg aac atc ttc ggc tgc aag ttc agc ctg aag aac   2832
Ser Ile Leu Gly Met Asn Ile Phe Gly Cys Lys Phe Ser Leu Lys Thr
    930                 935                 940

gac aac gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg   2880
Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
945                 950                 955                 960

tgg gcc atc atc acc gtg ttc atc atc atg gcc cag gag gac tgg aac   2928
Trp Ala Ile Val Thr Val Phe Ile Ile Met Ala Glu Glu Asp Trp Asn
                965                 970                 975

gtg tac ctg tac aac ggc atg gcc tcc acc tcc tgg gcc ctc aac ctc   2976
Val Tyr Leu Tyr Asn Gly Met Ala Ser Thr Ser Trp Ala Leu Asn Leu
            980                 985                 990

tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg   3024
Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
        995                 1000                1005

ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac   3072
Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
    1010                1015                1020

aga ttc gac acg cac gag gac aag acg tcg gtc cac ttc gag cag gac   3120
Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
1025                1030                1035                1040

ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt ccc   3168
Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
                1045                1050                1055

ctg gcc gtg acc ttc aac ggc acc tgg agg gac gag gca gcc tgt ccc   3216
Leu Ala Val Thr Phe Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
            1060                1065                1070

ctc acc tca tca tgt gca cag ctg cca cgc ccc tgc cta ccc cca aga   3264
Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
        1075                1080                1085

gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg   3312
Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
    1090                1095                1100

gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctt cgg   3360
Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
1105                1110                1115                1120

cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg   3408
Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp
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                1125                1130                1135

agc agg cgg cgt tcc agc tgg agc agc gtg ggc cgt gcc cag cct caa  3456
Ser Arg Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
1140                1145                1150

gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag  3504
Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
1155                1160                1165

ggc aag ggc agc acc gac gac gaa gtt gag gac ggc agg gcg cgc tcc  3552
Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
1170                1175                1180

ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg  3600
Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
1185                1190                1195                1200

ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg  3648
Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
1205                1210                1215

cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac  3696
Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
1220                1225                1230

cgc gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc  3744
Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
1235                1240                1245

ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg  3792
Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
1250                1255                1260

agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac  3840
Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
1265                1270                1275                1280

cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat  3888
Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
1285                1290                1295

cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg  3936
His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
1300                1305                1310

gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc  3984
Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
1315                1320                1325

gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg  4032
Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
1330                1335                1340

aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gtc tac ctg cag  4080
Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Val Tyr Leu Gln
1345                1350                1355                1360

agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg  4128
Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
1365                1370                1375

gac att gtc gtg gcc atg gcc tcg gat ggt ggc gcc aag atc ctg ggt  4176
Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
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                1380                1385                1390

gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cgc ctg agg gtc   4224
Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Arg Leu Arg Val
        1395                1400                1405

atc agc cgg gcc ccg ggc ttc aag ctg gtg gtg gag acg ctg ata tca   4272
Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
    1410                1415                1420

tca gtc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc   4320
Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
1425                1430                1435                1440

atc att ttt ggn att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac   4368
Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
                1445                1450                1455

tac tgc gag ggc ccc gac aan agg aac atc tcc acn aag gca cag tgc   4416
Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
            1460                1465                1470

cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac   4464
Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
        1475                1480                1485

ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat ggg   4512
Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
    1490                1495                1500

tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac aag   4560
Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
1505                1510                1515                1520

cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc   4608
Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
                1525                1530                1535

ttc ctg ctc atc gtc agc ttc ttt gtg ctg aac atg ttc gtg ggc gtc   4656
Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
            1540                1545                1550

gtg gtc gag aac ttt cac aag tgc cgg ccg cac cag gag gcg gag gag   4704
Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
        1555                1560                1565

gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag cgg agg cgc   4752
Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
    1570                1575                1580

agg agc act ttc acc agc cca gag gcc cag cgc cgg ccc tac tat gcc   4800
Arg Ser Thr Phe Pro Ser Pro Glu Ala Gln Arg Arg Pro Tyr Tyr Ala
1585                1590                1595                1600

gac tac tcg ccc acg cgc cgc tgg att cac tcg ctg tgc acc agc cac   4848
Asp Tyr Ser Pro Thr Arg Arg Trp Ile His Ser Leu Cys Thr Ser His
                1605                1610                1615

tac ctc gac ctc ttc atc acc ttc atc atc tgt gtc aac gtc atc acc   4896
Tyr Leu Asp Leu Phe Ile Thr Phe Ile Ile Cys Val Asn Val Ile Thr
            1620                1625                1630

atg tcc atg gag cac tat aac cax cnn aag tcg ctg gac gag gcc ctc   4944
Met Ser Met Glu His Tyr Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu
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                1635                1640                1645

aag aac cgc aac tac gtc ttc acc atc gtg ttt gtc tcc gag gct gma   4992
Lys Tyr Cys Asn Tyr Val Phe Thr Ile Val Phe Val Phe Glu Ala Ala
    1650                1655                1660

ctg aag ctg gta gca ttt ggg ttc cgt cgg ttt ttc aag gac agg tgg   5040
Leu Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp
1665                1670                1675                1680

aac cag ctg gac ctg gcc atc gtg ctg ctg tca ttt gtg ggc atc acg   5088
Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Leu Met Gly Ile Thr
                1685                1690                1695

ctg gag gag ata gag atg agc gcc gcg ctg ccc atc aac ccc acc atc   5136
Leu Glu Glu Ile Glu Met Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile
            1700                1705                1710

atc cgc atc atg cgc gtg ctt cgc att gcc cgt gtg ctg aag ctg ctg   5184
Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu
        1715                1720                1725

aag atg gct acg ggc atg cgc gcc ctg ctg gac act gtg gtg caa gct   5232
Lys Met Ala Thr Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala
    1730                1735                1740

ctc ccc cag gtg ggg aac ctg ggc ctt ctc ttc atg ctc ctg ttt ttt   5280
Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe
1745                1750                1755                1760

atc tat gct gcg ctg gga gtg gag ctg ttc ggg agg ctg gag tgc agt   5328
Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe Gly Arg Leu Glu Cys Ser
                1765                1770                1775

gaa gac aac ccc tgc gag ggc ctg agc agg cac gcc acc ttc agc aac   5376
Glu Asp Asn Pro Cys Glu Gly Leu Ser Arg His Ala Thr Phe Ser Asn
            1780                1785                1790

ttc ggc atg gcc ttc ctc acg ctg ttc cgc gtg tcc acg ggg gac aac   5424
Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn
        1795                1800                1805

tgg aac ggg atc atg aag gac acg ctg cgc gag tgc tcc agt gag gac   5472
Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp
    1810                1815                1820

aag cac tgc ctg agc tac ctg cag gac aag tcg cac gtc tac ttc gtg   5520
Lys His Cys Leu Ser Tyr Leu Gln Asp Lys Ser His Val Tyr Phe Val
1825                1830                1835                1840

acc ttc gtg ctg gtg ccc cag ttc gtg ctg gtg aac gtg gtg gtg gcc   5568
Thr Phe Val Leu Val Pro Gln Phe Val Leu Val Asn Val Val Val Ala
                1845                1850                1855

gtg ctc atg aag cac ctg gag gag agc aac aag gag gct cgg gag gac   5616
Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp
            1860                1865                1870

gcg gag ctg gac gcc gag atc gag ctg gag ctg gcg cag ggc aac ggg   5664
Ala Glu Leu Asp Ala Glu Ile Glu Leu Glu Leu Ala Gln Gly Pro Gly
        1875                1880                1885

agt gca cgc cgg gtg gac gcg gac agg ccc ccc ttg ccc cag gag agc   5712
Ser Ala Arg Arg Val Asp Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser
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      1890                1895                1900

ggg ggc gcc agg gat gtt cta aac ctg gtt gcc cgc aag gtg tcc gtg  5760
Pro Gly Ala Arg Asp Ala Pro Asn Leu Val Ala Arg Lys Val Ser Val
1905                1910                1915                1920

tcc agg atg ctc tcg ctg cgc aac gac agc tac atg ttc agg ccc gtg  5808
Ser Arg Met Leu Ser Leu Arg Asn Asp Ser Tyr Met Phe Arg Pro Val
                1925                1930                1935

gtg cct gcc tcg gcg ccc cac ccc cgc cag atg cag gag gtg gag atg  5856
Val Pro Ala Ser Ala Pro His Pro Arg Pro Leu Gln Glu Val Glu Met
            1940                1945                1950

gag acc tat ggg gcc ggc acc ccc ttg ggc tcc gtt gcc tct gtg cac  5904
Glu Thr Tyr Gly Ala Gly Thr Pro Leu Gly Ser Val Ala Ser Val His
        1955                1960                1965

tct ccg ccc gga gag tcc tgt gcc tcc ctc cag atc cca atg gct gtg  5952
Ser Pro Pro Ala Glu Ser Cys Ala Ser Leu Gln Ile Pro Leu Ala Val
    1970                1975                1980

tcg tcc ccc agc agg agc ggc gag ccc atc cac gcc ctg tcc cct cgg  6000
Ser Ser Pro Ala Arg Ser Gly Glu Pro Leu His Ala Leu Ser Pro Arg
1985                1990                1995                2000

ggc aca gcc cgc tcc ccc agt ctc agc cgg ctg ctc tgc aga cag gag  6048
Gly Thr Ala Arg Ser Pro Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu
                2005                2010                2015

gat gtg cac acc gat tcc ttg aag ggg aga ttg aca gcc cta ggg aca  6096
Ala Val His Thr Asp Ser Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr
            2020                2025                2030

ccc tgg atc ctg cag agc ctg gtg aga aaa ccc cgg                  6132
Pro Trp Ile Leu Gln Ser Leu Val Arg Lys Pro Arg
        2035                2040
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Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly
  1               5                  10                  15

cgc ngc ccc tgg ccc tgc ggn grt ggt ggg ggc gtc ccc gga gag ccc   96
Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
            20                  25                  30

cgg ggn gcc ggg acg nga ggc gga ggg ggg ttc gag ctc ggc gtg tca  144
Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
        35                  40                  45

ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac  192
Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
    50                  55                  60
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gag gag cag cgc gtc ccg tac ccg gcc ttj gcg gcc acg gtc ttc ttc  240
Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
 65                  70                  75                  80

tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc  288
Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
                 85                  90                  95

tgc aac cca tgg ttc gag cac gtg agc atg ccg gta atc atg ctc aac  336
Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn
            100                 105                 110

tgc gtg acc ctg ggc atg ttc agg ccc tgt gag gac gtt gag tgc ggc  384
Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys Gly
        115                 120                 125

tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc  432
Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
    130                 135                 140

ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc  480
Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
145                 150                 155                 160

ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc  528
Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
                165                 170                 175

atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg  576
Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
            180                 185                 190

agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc  624
Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
        195                 200                 205

atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat  672
Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
    210                 215                 220

acg ctg ccc atg ctc ggg aac gtc atc atg ctg tgc ttc ttc gtc ttc  720
Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
225                 230                 235                 240

ttc att ttc ggc atc gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg  768
Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                245                 250                 255

aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc  816
Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
            260                 265                 270

ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc  864
Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
        275                 280                 285

atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc  912
Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
    290                 295                 300

ccc ggc cgc cgc cgc gac gtg cgc atg aac tgc acc ctg ggc tgg gag gcc  960
Pro Gly Arg Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
305                 310                 315                 320
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tac acg cag ccg cag gcc gag ggg gtg ggc gct gca cgc aac gcc tgc  1008
Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
            325                 330                 335

atc aac tgg aac cag tac tac aac gtg tgc cgc tcg ggc gac tcc aac  1056
Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
        340                 345                 350

ccc cac aac ggt gcc atc aac ttc gac aac acc tgc tac gcc tgg att  1104
Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
    355                 360                 365

gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac atc atg tac  1152
Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr
370                 375                 380

tac gtc atg gac gcc aac tca ttc tac aac ttc atc tat ttc atc ctg  1200
Tyr Val Met Asp Ala Asn Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
385                 390                 395                 400

ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg  1248
Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
                405                 410                 415

att gcc atg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg  1296
Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
            420                 425                 430

cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc  1344
Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
        435                 440                 445

ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc  1392
Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
    450                 455                 460

cac ata ttc cgt aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc  1440
His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
465                 470                 475                 480

tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc  1488
Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                485                 490                 495

cag ggt ccc ggg cac agc cgc cgg gca ggc agg cac aca gcc tcg  1536
Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
            500                 505                 510

gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac  1584
Val His His Leu Val Tyr His His His His His His His His His Tyr
        515                 520                 525

cat ttc agt cat ggc agg ccc agc agg ccc ggc ccc gag cca ggc gcc  1632
His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
    530                 535                 540

tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc  1680
Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
545                 550                 555                 560

cca ggc cgc ggc ggg ccc ccc gac gcc gag tct gtg cac agc atc tac cat  1728
Pro Gly Arg Gly Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                565                 570                 575
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gcc gat tgt cac atc gag ggg ccg cag gag agg gcc cgg gtg ggc aca  1776
Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
            580                 585                 590

tgc cgc agc cac tgc cgc tgc cag ccc cag gct ggc cac agg gct ggg  1824
Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
        595                 600                 605

cac cat gaa ctc ccc cac gac cct gcc ctc agg ggt ggg cag cgg caa  1872
His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
    610                 615                 620

agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc  1920
Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala
625                 630                 635                 640

agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac  1968
Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
                645                 650                 655

gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa ggc ccc  2016
Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro
            660                 665                 670

ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc ccA  2064
Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
        675                 680                 685

gcg ggc aca crg acc tgt gag ctg aag agc tgt ccg tac tgc acc cgt  2112
Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
    690                 695                 700

gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac  2160
Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
705                 710                 715                 720

tta gat ggc cgt ggc gtc tac gaa ttc acg cag gac gtc cgg cac ggt  2208
Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                725                 730                 735

gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac acA ccA ggc  2256
Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
            740                 745                 750

cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca ggc acg  2304
Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
        755                 760                 765

ggc gag cca ggc tgg atg ggc ccc crc tgg grt acc ttc agc ggc aag  2352
Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
    770                 775                 780

ctg cgc cgc atc gtg gac agc aag tac ttc agt cgt ggc atc atg atg  2400
Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
785                 790                 795                 800

gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag  2448
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                805                 810                 815

ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc  2496
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
            820                 825                 830
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agt atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgt ggg ccc  2544
Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
        835                 840                 845

ctg ggc tac atc cgg aac ccg tat aac atc ttc gac ggc atc atc gtg  2592
Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
    850                 855                 860

gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tcc  2640
Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser
865                 870                 875                 880

gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttt  2688
Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
                885                 890                 895

ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac  2736
Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp
            900                 905                 910

aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc  2784
Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
        915                 920                 925

agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc atg aag acg  2832
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr
    930                 935                 940

gac act gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg  2880
Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
945                 950                 955                 960

tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac  2928
Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn
                965                 970                 975

gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tgg gcc gcc ctc
Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu
            980                 985                 990

tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg  3024
Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
        995                 1000                1005

ctg grg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc cat gcc aac  3072
Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
    1010                1015                1020

aga tcn gac acg gac gag gac aag acg tcg gtc cac ttc gag gag gac  3120
Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
1025                1030                1035                1040

ttc cac aag ctc aga gaa ctn cag acc aca gag ctg aag atg tgt tcc  3168
Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
                1045                1050                1055

ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc  3216
Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
            1060                1065                1070

ctn ccc tca tca tgt gca cag ctg cca ggc cca tgn cna ccc cca agn  3264
Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
        1075                1080                1085
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gat cac cac tcc tgg atg cag ccc cca gcc tcc cag acc ctc ggc gtg 3312
Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
1090 1095 1100

gca gaa gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg 3360
Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
1105 1110 1115 1120

cag cct ccg aag ttt tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg 3408
Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp
1125 1130 1135

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Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
1140 1145 1150

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Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
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Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
1170 1175 1180

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Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
1185 1190 1195 1200

ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg 3648
Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
1205 1210 1215

cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac 3696
Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
1220 1225 1230

cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tga tgc 3744
Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
1235 1240 1245

ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg 3792
Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
1250 1255 1260

agt agg agg cct ggg nnn tnt acc ctc tac nnn ttt tnc nna cag aac 3840
Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
1265 1270 1275 1280

cgg ttc cgc gtc tcc tgc cag aag gtc atc acn cac aag atg ttt gat 3888
Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
1285 1290 1295

cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc crg 3936
His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
1300 1305 1310

gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc 3984
Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
1315 1320 1325

gtc tcc aat tac atc ttc acg gcc atc ttc gtg gag gag atg atg gtg 4032
Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
1330 1335 1340

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aag gtg gtg gcc ctg ggg ctg ctg ttt ggc gag cac ggc tac ctg cag  4080
Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln
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agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg  4128
Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
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gac atc gcc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt  4176
Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
            1380                1385                1390

gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtg  4224
Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val
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atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca  4272
Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
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tca ctc agg ccc att ggg aac atc gtc ctc acc tgc tgc gcc ttc ttc  4320
Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
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atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac  4368
Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
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tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc  4416
Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
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cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac  4464
Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
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ctg ggc cag gtc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga  4512
Leu Gly Gln Val Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
    1490                1495                1500

tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag  4560
Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
1505                1510                1515                1520

cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc  4608
Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
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ttt ctg ctc atc gtc agt tac ttc gtg ctc aac atg ttc gtg ggc gtc  4656
Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
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gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag  4704
Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
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gcg cgg cgg cga gag gag aag cgg ctg cgg cgc ctg gag agg agg cgc  4752
Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
    1570                1575                1580

agg aag gcc cag cgc cgg ccc tac tat gcc gac tac tag ccc acg cgc  4800
Arg Lys Ala Gln Arg Arg Pro Tyr Tyr Ala Asp Tyr Ser Pro Thr Arg
1585                1590                1595                1600
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Arg Trp Ile His Ser Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile
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acc ttc atc att tgt gtc aac gtc atc acc atg tcc agg gag cac tat 4896
Thr Phe Ile Ile Cys Val Asn Val Ile Thr Met Ser Met Glu His Tyr
1620 1625 1630

aac caa ccc aag tcg atg gac gag gcc ctc aag tac tgc aac tac gtc 4944
Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu Lys Tyr Cys Asn Tyr Val
1635 1640 1645

ttc acc atc gtg ttt gtc ttc gag gct gca ctg aag ctg gta gcc ttt 4992
Phe Thr Ile Val Phe Val Phe Glu Ala Ala Leu Lys Leu Val Ala Phe
1650 1655 1660

ggg ttc cgt cgg ttc ttc aag gac agg tgg aac cag ctg gac ctg gcc 5040
Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp Asn Gln Leu Asp Leu Ala
1665 1670 1675 1680

atc gtg ctg ctg tca ctc atg ggc atc acg ctg gag gag ata gag atg 5088
Ile Val Leu Leu Ser Leu Met Gly Ile Thr Leu Glu Glu Ile Glu Met
1685 1690 1695

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Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val
1700 1705 1710

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Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr Gly Met
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Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val Gly Asn
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Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly
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Val Glu Leu Phe Gly Arg Leu Glu Cys Ser Glu Asp Asn Pro Cys Glu
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Gly Leu Ser Arg His Ala Thr Phe Ser Asn Phe Gly Met Ala Phe Leu
1780 1785 1790

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Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys
1795 1800 1805

gac acg ctg cgc gag tgc tcc cgt gag gac aag cac tgc ctg agc tac 5472
Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp Lys His Cys Leu Ser Tyr
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Leu Pro Ala Pro Ser Pro Val Tyr Phe Val Thr Phe Val Leu Val Pro
1825 1830 1835 1840

cag ttc gtg ctg gtg aac gtg gtg gtg gcc gtg ctc aag aag cac ctg 5568
Gln Phe Val Leu Val Asn Val Val Val Ala Val Leu Met Lys His Leu
1845 1850 1855

gaq gag agc aac aag gag gct cag gag gat gcg gag ctg gat gcc gag 5616
Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp Ala Glu Leu Asp Ala Glu
1860 1865 1870

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Ile Glu Leu Glu Met Ala Gln Gly Pro Gly Ser Ala Arg Arg Val Asp
1875 1880 1885

gcg gac agg cct ccc ttg ccc cag gag agt ccg ggc gcc agg gac gcc 5712
Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser Pro Gly Ala Arg Asp Ala
1890 1895 1900

cca aac ctg gtt gca cgc aag gtg tcc gtg tcc agg atg ctc tcg ctg 5760
Pro Asn Leu Val Ala Arg Lys Val Ser Val Ser Arg Met Leu Ser Leu
1905 1910 1915 1920

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Pro Asn Asp Ser Tyr Met Phe Arg Pro Val Val Pro Ala Ser Ala Pro
1925 1930 1935

cac ccc cgc cag ctg cag gag gtg gag atg gag acc tat ggg gcc ggc 5856
His Pro Arg Pro Leu Gln Glu Val Glu Met Glu Thr Tyr Gly Ala Gly
1940 1945 1950

acc ccc ttg ggc tcc gtt gcc tct gtg cac tcc acg ccc gca gag tcc 5904
Thr Pro Leu Gly Ser Val Ala Ser Val His Ser Pro Pro Ala Glu Ser
1955 1960 1965

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Cys Ala Ser Leu Gln Ile Pro Leu Ala Val Ser Ser Pro Ala Arg Ser
1970 1975 1980

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Gly Glu Pro Leu His Ala Leu Ser Pro Arg Gly Thr Ala Arg Ser Pro
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Ala Glu Pro Gly Val Thr Thr Glu Gln Pro Gly Thr Arg Ser Pro Pro
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Ser Ser Pro Pro Gly Leu Glu Glu Pro Leu Asp Gly Ala Asp Pro His
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gtc cca cac cca gag ctg gtg cct att gcc ttc tac tgc ctg cga cag      192
Val Pro His Pro Asp Leu Ala Pro Ile Ala Phe Phe Cys Leu Arg Gln
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acc acc agc ccc cgg aac tgg tgc atc aag atg gtg tgc aac ccg tgg      240
Thr Thr Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp
65                  70                  75                  80

ttt gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt      288
Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu
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Gly Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys
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aag atc atg cag gtc ttt gat gac ttc atc ttt atc ttc ttc ttc gcc atg      384
Lys Ile Met Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Phe Ala Met
        115                 120                 125

gag atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc      432
Glu Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys
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tac ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca      480
Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala
145                 150                 155                 160

ggg atg gtc gag tac tcc ctg gac ctt cag aac atc aac ctg tca gcc      528
Gly Met Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala
                165                 170                 175

atc cgc acc gtg cgc gtc ctg agg ccc ctc aaa gcc atc aac cgc gtg      576
Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val
            180                 185                 190

ccc agt atg cgg atc ctg gtg aac ctg ctc ctg gac acg ctg gcc atg      624
Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met
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Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly
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Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe
225                 230                 235                 240

ctg gag gag aac ttc acc ata caa ggg gat gtg gcc tcg ccc ccg tcc      768
Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Ser
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tac cag ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg acg      816
Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser
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Gly Asp Asp Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu
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cag ggc cgt gag tgc tgc cag ctg tcc aag gac gac gtg tac gac ttc ggg      912
Gln Gly Arg Glu Cys Cys Gln Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly
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gcg ggg cgc cag gac ctc aat gcc agc ggc ctg tgt gtc aac tgg aac      960
Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn
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cgt tac tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt     1008
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly
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gcc atc aac ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag     1056
Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln
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Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
        355                 360                 365

gct cac ccc ttc tac aac ttt atc tac ttc atc gtt gtc atc ata gtg     1152
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val
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Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln
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ttt tcg gag acc aag caa cgg gag cac cgg ctg atg ctg gag cag cgg     1248
Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg
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Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly
            420                 425                 430

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Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys
        435                 440                 445

gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg cag agc cgg cgc     1392
Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg
    450                 455                 460

cag gcc ctg ggc ccg gag gcc ccg gcc ccc gcc aaa cct ggg ccc cac     1440
Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His
465                 470                 475                 480

gcc aag gag ccc cgg cac tac cag ctg tgc ccg caa cat agc ccc ctg     1488
Ala Lys Glu Pro Arg His Tyr Gln Leu Cys Pro Gln His Ser Pro Leu
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gat gcg acg ccc cac ccc acc ctg gtg cag acc atc acc gcc acg ctg gct     1536
Asp Ala Thr Pro His Pro Thr Leu Val Gln Thr Ile Thr Ala Thr Leu Ala
            500                 505                 510

tcc gat ccc gcc agc tgc cct tgc tgc cag cat gag gac ggc cgg cgg     1584
Ser Asp Pro Ala Ser Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg
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Glu Thr Arg Ala Lys Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn
595 600 605

cgg ggc atc atg atg gcc atc ctg gtc aac acc gcc gcc agc atg ggc atc 1872
Arg Gly Ile Met Met Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile
610 615 620

gag cac cac gag cag ccg gag cag ctg acc aac atc ctg gag atc tgc 1920
Glu His His Glu Gln Pro Glu Gln Leu Thr Asn Ile Leu Glu Ile Cys
625 630 635 640

aat gtg gcc ttc acc agc atg ttt gcc ctg gag atg atc ctg aag ctg 1968
Asn Val Val Phe Thr Ser Met Phe Ala Leu Glu Met Ile Leu Lys Leu
645 650 655

gcc gcc ttt ggg ctc ttc gac tac ctg cgt aac ccc tac aac atc ttc 2016
Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn Ile Phe
660 665 670

gac agc atc att gtc atc atc agc atc tgg gag atc gtg ggg cag gcg 2064
Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly Gln Ala
675 680 685

gac ggt ggg ctg tcg gtg ctg cgg acc ttc cgg ctg ctg cgc gtg ctg 2112
Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu
690 695 700

aaa ctg gtg cgc ttc atg cct gcc ctg cgg cgc cag ctc gtg gtg atc 2160
Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val Val Leu
705 710 715 720

atg aag acc atg gac aac gtg gcc acc ttc tgc atg ctg ctc atg atc 2208
Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu
725 730 735

ttc atc ttc atc ttc agc atc ctt ggg atg cat att ttt ggc tgc aag 2256
Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly Cys Lys
740 745 750

ttc agc ctg cgc acg gac act gga gac acg gtg ccc gac agg aag aac 2304
Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn
755 760 765

ttc gac tct ctg ctg tgg gcc atc gtc act gtg ttc cag atc ctc acc 2352
Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr
770 775 780

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cag gag gac tgg aac gtc gtt cta tac aat ggc agg gcc tcc act tct  2400
Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser
785                 790                 795                 800

ccc agg gcc tgc ctc tac ttt gtc gct gtc atg acc ttt gga aac tat  2448
Pro Trp Ala Ser Leu Tyr Phe Val Ala Val Met Thr Phe Gly Asn Tyr
                805                 810                 815

gtg ctc ttc aac ctg ctg gcg gct atc ctg gtg gag ggc ttt cag gcg  2496
Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala
            820                 825                 830

gag ggc gac gcc aat cgc tcc tac tcg gac gag gac cag agc tca tct  2544
Glu Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser Ser Ser
        835                 840                 845

aac ata gaa gag ttc gat aag ctc cag gaa ggc ctg gac agc agc ggg  2592
Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser Gly
    850                 855                 860

gat ccc aag ctc tgc cca atc ccc atg acc ccc aat gag cac ctg gac  2640
Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Glu His Leu Asp
865                 870                 875                 880

ccc agt ctc cca ctg ggt ggg cac gtc ggt cct ggg ccc gcg ggc gga  2688
Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala Gly
                885                 890                 895

cct gcc ccc cgg ctc tca ctg cag ccg gac ccc atg ctg gtg gcc ctg  2736
Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala Leu
            900                 905                 910

ggc tcc cga aag agc agc gtc atg tct cta ggg agg atg agc tat gac  2784
Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser Tyr Asp
        915                 920                 925

cag cgc tcc ctg tcc agc tcc cgg agc tcc tac tac ggg cca tgg ggc  2832
Gln Arg Ser Leu Ser Ser Ser Arg Ser Ser Tyr Tyr Gly Pro Trp Gly
    930                 935                 940

cgc agc gcg gcc tgg gcc agc cgt cgc tcc agc tgg aac agc ctc aag  2880
Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser Ser Trp Asn Ser Leu Lys
945                 950                 955                 960

cac aag ccg ccg tcg gcg gag cat gag tcc ctg ctc tct gcg gag cgc  2928
His Lys Pro Pro Ser Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg
                965                 970                 975

ggc ggc ggc gcc cgg gtc tgc gag gtt gcc gcg gcc gag ggg ccg ccg  2976
Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro
            980                 985                 990

cgg gcc gca ccc ctg cac acc cca cac gcc cac cac gtt cat cac ggg  3024
Arg Ala Ala Pro Leu His Thr Pro His Ala His His Val His His Gly
        995                1000                1005

ccc cat ctg ggg cac cgc cac cgc cac cac cgc agg acg ctg tcc ctc  3072
Pro His Leu Gly His Arg His Arg His His Arg Arg Thr Leu Ser Leu
    1010                1015                1020

gac aac agg gac tcg gtg gac ctg gcc gag ccg gtg ccc gcg gtg ggc  3120
Asp Asn Arg Asp Ser Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly
1025                1030                1035                1040
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gct cac tct cgg gcc gtc tgg agg gcg gca ggc ccg gcc ccc ggg cat  3168
Ala His Ser Arg Ala Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His
            1045                1050                1055

gag gac tgc aac ggc agg atg ccc agc atc gcc aaa gac gtc ttc acc  3216
Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr
        1060                1065                1070

aag atg ggc gac cgc ggg gat cgc ggg gag gat gag gag gaa atc gac  3264
Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp
    1075                1080                1085

tac acc ctg tgc ttc cgt gtc cgc aag atg atc gac gtc tat aag ccc  3312
Tyr Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro
1090                1095                1100

gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc  3360
Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro
1105                1110                1115                1120

gag aac agg ttc cgg gtc ctg tgt cag acc atc att gcc cac aaa ctc  3408
Glu Asn Arg Phe Arg Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu
                1125                1130                1135

ttc gac tac gtc gtc ctg gcc ttc atc ttt ccc aac tgc atc acc atc  3456
Phe Asp Tyr Val Val Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile
            1140                1145                1150

gcc ctg gag cgg cct cag atc gag gcc ggc agc acc gaa cgc atc ttt  3504
Ala Leu Glu Arg Pro Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe
        1155                1160                1165

atc aac gtg tcc aac tac atc ttc acg gcc atc ttc gtg ggc gag atg  3552
Leu Thr Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met
    1170                1175                1180

aca ttg aag gta gtc ttg gtg ggc ctg tac ttc ggc gag cag gcg tac  3600
Thr Leu Lys Val Val Ser Leu Gly Leu Tyr Phe Gly Gln Gln Ala Tyr
1185                1190                1195                1200

cta cgc agc agc tgg aac gtg ctg gat ggc ttt ctt gtc ttc gtg tcc  3648
Leu Arg Ser Ser Trp Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser
                1205                1210                1215

atc atc gac atc gtg gtg tcc ctg gcc tca gcc ggg gga gcc aag atc  3696
Ile Ile Asp Ile Val Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile
            1220                1225                1230

ttg ggg gtc ctc cga gtc ttg cgg ctc ctg cgc acc cta cgc ccc ctg  3744
Leu Gly Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu
        1235                1240                1245

cgt gtc atc agc cgg gcg ccg ggc ctg aag ctg gtg gtg gag aca ctc  3792
Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu
    1250                1255                1260

atc tcc tcc ctc aag ccc atc ggc aac atc gtg ctc atc tgc tgt gcc  3840
Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala
1265                1270                1275                1280

ttc ttc atc atc ttt ggc atc ctg gga gtg cag ctt ttc aag ggc aag  3888
Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys
                1285                1290                1295
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ttc tat cat tgt ctg ggc gtg gac acc ggc aac atc acc aat tgc tag                3936
Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile Thr Asn Arg Ser
        1300                1305                1310

gcc tgt atg gcc gcc aac tac tgc tgg ctg cac cac aaa tac aat ttt                3984
Asp Cys Met Ala Ala Asn Tyr Arg Trp Val His His Lys Tyr Asn Phe
    1315                1320                1325

gac aac ctg ggc cag gct ctg atg tcc ctc ttt gtc ctg gca tcc aag                4032
Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ala Ser Lys
1330                1335                1340

gat ggt tgg gtg aac atc atg tac aat gga ctg gat gct gtt gct gtg                4080
Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp Ala Val Ala Val
1345                1350                1355                1360

gat cag cag cct gtg acc aac cac aac ccc tgg atg ctg ctg tac ttc                4128
Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met Leu Leu Tyr Phe
                1365                1370                1375

atc tcc ttc ctg ctc atc gtc agc ttc ttt gtg ctc aac atg ttt gtg                4176
Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val
            1380                1385                1390

ggt gtc gtg gtg gag aac ttc cac aag tgc cgg cag cac cag gag gct                4224
Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln His Gln Glu Ala
        1395                1400                1405

gaa gag gca cgg cgg cgt gag gag aag cgg ctg cgg cgc ctg gac aag                4272
Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys
    1410                1415                1420

aag cgc cgg aag gcc cag cgg ctg ccc tac tat gcc acc tat tgt cac                4320
Lys Arg Arg Lys Ala Gln Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys His
1425                1430                1435                1440

acc cgg ctg ctc atc cac tcc atg tgc acc agc cac tac ctg gac atc                4368
Thr Arg Leu Leu Ile His Ser Met Cys Thr Ser His Tyr Leu Asp Ile
                1445                1450                1455

ttc atc acc ttc atc atc tgc ctc aac gtg gtc acc atg tcc ctg gag                4416
Phe Ile Thr Phe Ile Ile Cys Leu Asn Val Val Thr Met Ser Leu Glu
            1460                1465                1470

cac tac aat cag ccc acg tcc ctg gag gca gcc ctc aag tac tgc aac                4464
His Tyr Asn Gln Pro Thr Ser Leu Glu Thr Ala Leu Lys Tyr Cys Asn
        1475                1480                1485

tat atg ttc acc act gtc ttt gtg ctg gag gct gtg ctg aag ctg gtg                4512
Tyr Met Phe Thr Thr Val Phe Val Leu Glu Ala Val Leu Lys Leu Val
    1490                1495                1500

gca ttt ggt ctg agg cgc tta ttt aag gac cga tgg aac cag ctg gac                4560
Ala Phe Gly Leu Arg Arg Arg Leu Phe Lys Asp Arg Trp Asn Gln Leu Asp
1505                1510                1515                1520

ctg gcc att gtg cta ctg tca gtc atg ggc atc acc ctg gag gag atc                4608
Leu Ala Ile Val Leu Leu Ser Val Met Gly Ile Thr Leu Glu Glu Ile
                1525                1530                1535

gag atc aat gcg gcc ctg ccc atc aat ccc acc atc atc cgc atc atg                4656
Glu Ile Asn Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met
            1540                1545                1550
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agg gtt cag cgc att gcc cga gtc cag aag ctg ttg gag atg gcc aac      4704
Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr
        1555                1560                1565

gga atg cgg gcc ctg ctg gac acg gtg gtg caa gct ttg act cag gtg      4752
Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val
    1570                1575                1580

ggc aac ctg ggc ctc ctc ttc aag ctg ctc ttc ttc atc tat gct gct      4800
Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala
1585                1590                1595                1600

ctc ggg gtg gag ctc ttt ggg aag ctg gtc tgc aac gcc gag aac ccg      4848
Leu Gly Val Glu Leu Phe Gly Lys Leu Val Cys Asn Asp Glu Asn Pro
                1605                1610                1615

tgc gag ggc atg agc cgg cat gcc aca ttt gag aac ctc ggc atg gcc      4896
Cys Glu Gly Met Ser Arg His Ala Thr Phe Glu Asn Phe Gly Met Ala
            1620                1625                1630

ttc ctc aca ctc ttc cag gtc tcc acg ggt gac aac tgg aac ggg atc      4944
Phe Leu Thr Leu Phe Gln Val Ser Thr Gly Asp Asn Trp Asn Gly Ile
        1635                1640                1645

atg aag gac acg ctg cgg gac tgc acc cac gac gag cgc agt tgt ctg      4992
Met Lys Asp Thr Leu Arg Asp Cys Thr His Asp Glu Arg Ser Cys Leu
    1650                1655                1660

agc agc ctg cag ttt gtg tcg ccg ctg tac ttc gtg agc ttc gtg ctc      5040
Ser Ser Leu Gln Phe Val Ser Pro Leu Tyr Phe Val Ser Phe Val Leu
1665                1670                1675                1680

acc gcg cag ttc gtg ctc atc aac gtg gtg gtg gct gtg ctc atg aag      5088
Thr Ala Gln Phe Val Leu Ile Asn Val Val Val Ala Val Leu Met Lys
                1685                1690                1695

cac ctg gac gac agc aac aag gag gcg cag gag gac gcc gag atg gat      5136
His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp Ala Glu Met Asp
            1700                1705                1710

gcc gag ctc gag ctg gag atg gcc cat ggc ctg ggc cct ggc acg agg      5184
Ala Glu Leu Glu Leu Glu Met Ala His Gly Leu Gly Pro Gly Pro Arg
        1715                1720                1725

ctg cct acc ggc tcc acg ggc gcc cct ggc cga ggg ccg gga ggg gcg      5232
Leu Pro Thr Gly Ser Pro Gly Ala Pro Gly Arg Gly Pro Gly Gly Ala
    1730                1735                1740

ggc ggc ggg ggc gac acc gat ggc ggc ctg tgc cgg cgc tgc tac tcg      5280
Gly Gly Gly Gly Asp Thr Asp Gly Gly Leu Cys Arg Arg Cys Tyr Ser
1745                1750                1755                1760

cct gcc cag gag aac ctg tgg ctg gac agc gtc tct tta atc atc aag      5328
Pro Ala Gln Glu Asn Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys
                1765                1770                1775

gac tcc ttg gag ggg gag ctg acc atc atc gac aac ctg tcg ggc tcc      5376
Asp Ser Leu Glu Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser
            1780                1785                1790

atc atc cac cac tac tcc tgg cct gcc ggc tgc gag gag tgt cac cac      5424
Ile Phe His His Tyr Ser Ser Pro Ala Gly Cys Lys Lys Cys His His
        1795                1800                1805
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gat aac caa gag aca ggt ccc cgt cca tct tgt tgg gtg acg acc      5469
Asp Lys Gln Glu Thr Gly Pro Arg Pro Ser Cys Trp Val Thr Thr
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<222> (1)..(5505)

<400> 12

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Met Ala Asp Ser Asn Leu Pro Pro Ser Ser Ala Ala Ala Pro Ala Pro
  1               5                  10                  15

gag ccg gga atc act gag cag ccg ggg ccc cgg agt ccc cct cca tcc    96
Glu Pro Gly Ile Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro Pro Ser
            20                  25                  30

cct cta ggc ctg gag gag cca ttg gaa gga acc aac cct gac gtc cca   144
Pro Pro Gly Leu Glu Glu Pro Leu Glu Gly Thr Asn Pro Asp Val Pro
        35                  40                  45

cat cca gac ctg gct act gtt gct ttc ttc tgc ctg cgc cag acc aag   192
His Pro Asp Leu Ala Pro Val Ala Phe Phe Cys Leu Arg Gln Thr Thr
    50                  55                  60

agc cca cgg aac tgg tgc atc aag atg gtt tgt aac ccg tgg ttc gag   240
Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp Phe Glu
65                  70                  75                  80

tgt gtg agc atg ctg gtt att ctg ctg aac tgt gtg acc ctg ggc atg   288
Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met
                85                  90                  95

tac cag cca tgt gat gac atg gag tgc ctg tcg gac cgt tgc aag atc   336
Tyr Gln Pro Cys Asp Asp Met Glu Cys Leu Ser Asp Arg Cys Lys Ile
            100                 105                 110

ctg cag gtc ttc gat gac ttc atc ttc atc ttc ttt gcc atg gag atg   384
Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met
        115                 120                 125

gtg ctt aag atg gtg gcc ctg ggc att ttt ggc aag aag tgt tac ctc   432
Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu
    130                 135                 140

gga gat aca tgg aac cgc ctg gat ttc ttc att gtc atg gca ggg atg   480
Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Met
145                 150                 155                 160

gtt gag tac tct ctg gac cta cag aac atc aac ctg tca gcc atc cgc   528
Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala Ile Arg
                165                 170                 175

act gtg cgt gtc ctg agg cct ctc aaa gcc atc aac cgt gta ccc agc   576
Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val Pro Ser
            180                 185                 190

atg cgg atc ctg gtg aac ctg ctg ctc gac acg ctg ccc atg ctg ggc   624
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Met Arg Ile Leu Val Asp Leu Leu Leu Asp Thr Leu Pro Met Leu Gly
            195                 200                 205

aac gtg cct ctg ttc tgt ttc ttc gtc ttc ttc atc ttc ggc atc atc      672
Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile
    210                 215                 220

ggt gtg cag gtc tgg gca ggc ctg ctg cgg aac cgc tgc ttc ctg gac      720
Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
225                 230                 235                 240

gag aac ttc acc ata caa ggg gat gtg gcc ctg ccc cct tat tac caa      768
Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
                245                 250                 255

cca gag gag gat gac gag atg ccc ttt atc tgc tcc ctg act ggg gac      816
Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
            260                 265                 270

aat ggc atc atg ggc tgc cac gag atc ccc cca ctg aag gag cag ggc      864
Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
        275                 280                 285

cgg gaa tgc tgc ctg tcc aaa gat gat gtg tat gac ttc ggg gcg ggg      912
Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
    290                 295                 300

cgc cag gac ctc aac gcc agc ggt ctg tgc gtc aac tgg aac cgc tac      960
Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
305                 310                 315                 320

tac aac gtc tgc cgc aag ggc aac gcc aac cct cac aag ggc gcc atc     1008
Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile
                325                 330                 335

aac ttt gac aac att ggc tat gcc ggg att gtg att ttc cag gtg atm     1056
Asn Phe Asp Asn Ile Gly Tyr Ala Gly Ile Val Ile Phe Gln Val Ile
            340                 345                 350

act ctg gaa ggc tgg gtg gag atc atg tac tat gtg atg gac gca cat     1104
Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His
        355                 360                 365

tct ttc tac aac ttc att tac ttc att ctg ctc atc ata gtg ggc tcc     1152
Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser
    370                 375                 380

ttc ttc atg atc aac ttg tgc gtc gtt gtc ata gca acc cag ttc tct     1200
Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser
385                 390                 395                 400

gag acc aag caa agg gag cac cgg ctg atg ctg gag caa cgc cag cgc     1248
Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg Gln Arg
                405                 410                 415

tan crg tcc tcc agc ang gtg gcc agt tac gct gag ccc ggt gat tgc     1296
Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly Asp Cys
            420                 425                 430

tat gag gag atc ttc caa tat gtc tgt cac atc ctt cgc aaa gcc aag     1344
Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys Ala Lys
        435                 440                 445

cgc cgt gcc cta ggc ang aac cag gcc ctg cag aac cgg cgc cag gcc     1392
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Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Asp Arg Arg Gln Ala
    450                 455                 460

atg ggc cag ggg aca cca gcc cct gcc aag ctt ggg ccc cac gcc aag      1440
Met Gly Pro Gly Thr Pro Ala Pro Ala Lys Pro Gly Pro His Ala Lys
465                 470                 475                 480

gag cac agc cac tgc aag ctg tgc cca cga cac agc ccc atg gac ccc      1488
Glu Pro Ser His Cys Lys Leu Cys Pro Arg His Ser Pro Leu Asp Pro
                485                 490                 495

act ccc cac aca ctg gtg cag ccc acc tct gcc atc ctg gcc tct gac      1536
Thr Pro His Thr Leu Val Gln Pro Thr Ser Ala Ile Leu Ala Ser Asp
            500                 505                 510

ccc agc agc tgc cct cac tgc cag cac gag gca ggc agg cgg ccc tct      1584
Pro Ser Ser Cys Pro His Cys Gln His Glu Ala Gly Arg Arg Pro Ser
        515                 520                 525

ggc ctg ggc agc act gac tca ggc cag gaa ggc tca ggt tct ggt ggc      1632
Gly Leu Gly Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Gly
    530                 535                 540

tct gca gag gcc gaa gcc aat ggg gat gga ctc cag agc agt gag gat      1680
Ser Ala Glu Ala Glu Ala Asn Gly Asp Gly Leu Gln Ser Ser Glu Asp
545                 550                 555                 560

ggg gtc tcc tcg gac ctg ggg aag gag gag gaa cag gaq gac ggg gca      1728
Gly Val Ser Ser Asp Leu Gly Lys Glu Glu Glu Gln Glu Asp Gly Ala
                565                 570                 575

gcc cga ctg tgt ggg gat gtg tgg cgc gag aca cga aaa aag ctg cgg      1776
Ala Arg Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Lys Lys Leu Arg
            580                 585                 590

ggc atc atg gac agc aag tac ttc aac aga ggt atc atg atg aag gcc atc      1824
Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met Ala Ile
        595                 600                 605

ctg gtg aac aca gtc agc atg ggc atc gag cac cac gaa cag ccc gag      1872
Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln Pro Glu
    610                 615                 620

gag ctg acc aac atc ctg gag atc tgc aat gtg gtc ttc acc agt atg      1920
Glu Leu Thr Asn Ile Leu Glu Ile Cys Asn Val Val Phe Thr Ser Met
625                 630                 635                 640

ttt gcc ctg cag atg atc ctg aac ctg gcc gcc ttt ggg ctc ttc gac      1968
Phe Ala Leu Gln Met Ile Leu Lys Leu Ala Ala Phe Gly Leu Phe Asp
                645                 650                 655

tac ctg cgg aac cct tac aac atc ttt gac agc atc atc gtc atc atc      2016
Tyr Leu Arg Asn Pro Tyr Asn Ile Phe Asp Ser Ile Ile Val Ile Ile
            660                 665                 670

agc atc tgg gaa atc gtg ggg cag gcg gac ggt ggc ctg tat gtg ctg      2064
Ser Ile Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser Val Leu
        675                 680                 685

cgc acc ttc cgg ttg ctg cgg gtg ctg aag ctg gtg cgc ttc atg ccg      2112
Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe Met Pro
    690                 695                 700

gcg ctg cgg cgc cag atc gtg gtg ctc atg aag acc atg gac aac gcc      2160
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Ala Leu Arg Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn Val
 705                 710                 715                 720

ggt aca ttc tgc atg cta ctc agt cag ttt atc ttt ttc atc ttc agc atc      2208
Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser Ile
                725                 730                 735

ctt ggg atg cat atc ttt ggc tgt aaa ttc agc ctt cgc acg gac acg      2256
Leu Gly Met His Ile Phe Gly Cys Lys Phe Ser Leu Arg Thr Asp Thr
            740                 745                 750

gga gac aca gtt cct gac agg aag aac ttc gat tcc tta ctg tgg gcc      2304
Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
        755                 760                 765

atc gtc aca gtg ttc cag atc ctc act cag gag gac tgg aac gtt gtc      2352
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Val Val
    770                 775                 780

ctg tac aat ggc atg cgc tcc acc acc ccc tgg gcc tcc ctc tat ttt      2400
Leu Tyr Asn Gly Met Ala Ser Thr Thr Pro Trp Ala Ser Leu Tyr Phe
785                 790                 795                 800

gtt gcc ctc atg acc ttt ggc aac tac gtt ctg ttc aat gtc ctg gtg      2448
Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
                805                 810                 815

gct atc cug gta gag ggt ttc cag gct gag ggt gat gct aat cgt tcc      2496
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Arg Ser
            820                 825                 830

tgc tct gat gag gac cag agc tca tcc aat ttg gag gag ttt gac aag      2544
Cys Ser Asp Glu Asp Gln Ser Ser Ser Asn Leu Glu Glu Phe Asp Lys
        835                 840                 845

ctc cca gag ggc ctg gac aac agt aga gat ctc aag cnc tgc cca ata      2592
Leu Pro Glu Gly Leu Asp Asn Ser Arg Asp Leu Lys Leu Cys Pro Ile
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ccc atg aca ccc aat gga cac ctg gac cct agc ctc cct ctg ggt gcg      2640
Pro Met Thr Pro Asn Gly His Leu Asp Pro Ser Leu Pro Leu Gly Ala
865                 870                 875                 880

cat ctg ggt cct gct ggt acc atg agt act gcc ccc cgc ctc tca ctg      2688
His Leu Gly Pro Ala Gly Thr Met Gly Thr Ala Pro Arg Leu Ser Leu
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cag cca gac ccg gta ctg gtg gcc cta gac rat ggg aaa agc agt gtc      2736
Gln Pro Asp Pro Val Leu Val Ala Leu Asp Ser Arg Lys Ser Ser Val
            900                 905                 910

atg tcc ctg ggc agg atg agc tat gat cag cga tcc ttg tcc agc tcc      2784
Met Ser Leu Gly Arg Met Ser Tyr Asp Gln Arg Ser Leu Ser Ser Ser
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cgg agc tcc tac tac ggg ccc tgg ggc cgc agt ggg acc tgg gct agc      2832
Arg Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Gly Thr Trp Ala Ser
    930                 935                 940

cgc cgc tcc agc tgg aac agc ctg aaa cac aag ccg ccc tca gct gag      2880
Arg Arg Ser Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu
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cat gag tcc tta ctg tct ggg gag ggt gga ggt agc tgc gtc agg gcc      2928
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His Glu Ser Leu Leu Ser Gly Glu Gly Gly Gly Ser Cys Val Arg Ala
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tgt gaa ggc gcc cgg gag gag gcg aaa act cgc acg gta ccc cgg cat  2976
Cys Glu Gly Ala Arg Glu Glu Ala Pro Thr Arg Thr Ala Pro Leu His
            980                 985                 990

cgt ccs cac ycg cac cac gcg cac cat gga ccc cac ctg gca cac cgt  3024
Ala Pro His Ala His His Ala His His Gly Pro His Leu Ala His Arg
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cac cga cac cac cgc cgg act ctg tcc ctt gat acc agg gac tct gtt  3072
His Arg His His Arg Arg Thr Leu Ser Leu Asp Thr Arg Asp Ser Val
    1010                1015                1020

gac ctg gga gag ctg grg ccc gtg gtg ggt gcc cac tca agg gcc gct  3120
Asp Leu Gly Glu Leu Val Pro Val Val Gly Ala His Ser Arg Ala Ala
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Trp Arg Gly Ala Gly Gln Ala Pro Gly His Glu Asp Cys Asn Gly Arg
                1045                1050                1055

atg ccc aac ata gcc aag gat gtc ttc acc aag atg gat gac cgc cgc  3216
Met Pro Asn Ile Ala Lys Asp Val Phe Thr Lys Met Asp Asp Arg Arg
            1060                1065                1070

gac cgc ggg gag gac gag gag gag atc gac tat acm ctg tgt ttc cgg  3264
Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp Tyr Thr Leu Cys Phe Arg
        1075                1080                1085

gtc ngc aag atg att gat gtg tac aag ccg gac tgg tgc gaa gtc cgc  3312
Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp Cys Glu Val Arg
    1090                1095                1100

gag gac tgg tcg gtc tac ctc ttc tcc ccc gag aac aag ttc cgg atc  3360
Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu Asn Lys Phe Arg Ile
1105                1110                1115                1120

ctg tgt cag acc atc atc ggt cac aag ctt ttt gac tac gtg gtc ttg  3408
Leu Cys Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu
                1125                1130                1135

gcc ttt atc ttc ctc aac tgt atc acc att gct ctg gag aga ccc cag  3456
Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln
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att gaa gct ggt agc act gag cgc atc ttc ctc acg gtg tct aac tac  3504
Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr
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atc ttc acm gcc atc ttc gtg ggc gag atg aca ctg aag gtg gtt tct  3552
Ile Phe Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser
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ctg ggc ctg tac ttt ggt gag cag gcg tac ctg cgt agc agc tgg aac  3600
Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn
1185                1190                1195                1200

gta ctg gat ggt ttc ctg gtc ttt gtg tcn atc atc gat atc gta gtg  3648
Val Leu Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val
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Ser Val Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val
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ctg cgg atc ctg cgt acc gta cgt ttt ttg agg gtt atc agc cgg gcc   3744
Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala
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cct ggg ctg aag ctg ggg gta gag acg ttc atc tcc tcc ctc aag ccc   3792
Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro
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att ggg aac atc gtc ctc atc tgc tgt gcc ttc ttc atc atc ttc ggc   3840
Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly
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atc ctg ggg gtg cag ctt ttc aaa ggc aag ttc tac cat tgt ttg gga   3888
Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly
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gtg gac acc cga aac atc acc aac cga tcc gac tgc gtg gcg gcc aac   3936
Val Asp Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Val Ala Ala Asn
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tac aqn tgg gtg cat cac aaa tac aac ttt gac aac ctg ggc cag gca   3984
Tyr Arg Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala
        1315                1320                1325

ttg atg tcc ctc ttt gtc ttg gcc tcc aag gac ggc tgg gtg aac atc   4032
Leu Met Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile
    1330                1335                1340

atg tat aat gga tta gat gct gtt gct gtg gac cag cag cca gtg acg   4080
Met Tyr Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr
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aac cac aac ccc tgg atg cta ctg tac ttc att tcg ttc ctg ctc atc   4128
Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile
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gtc agc ttc ttt gtg ctc aac atg ttt gtg ggc gtg gtc gtg gag aac   4176
Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn
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ttc cac aag tgc cgg cag cac cag gag gct gag gag gcg cgg agg cgt   4224
Phe His Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg
        1395                1400                1405

gag gag aaa cgg ctg cgg cgc ctg gaa aag aag cgc cgt aag gct cag   4272
Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln
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agg ctg ccc tac tat gct acc tac tgt ccc acg agg ctg ttc atc cac   4320
Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys Pro Thr Arg Leu Leu Ile His
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tcc atg tgc acc agc cac tac ctg gac atc ttc atc acc ttc atc atc   4368
Ser Met Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile
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tgc ctg aat gtt gtc acc atg tcc ctg gag cac tac aac cag cct acc   4416
Cys Leu Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
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tcc ctc gag acc gtc ctt aag tac tgc aac tac atg ttc acc aat gtc   4464
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ttt gtg ctg gag gct gtg ctg aag ctg gtg gca ctt ggc ctg agg agt  4512
Phe Val Leu Glu Ala Val Leu Lys Leu Val Ala Phe Gly Leu Arg Arg
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ttc ttc aag gac cga tgg aac cag ctg gac ctg gct att gtg ctg ctg  4560
Phe Phe Lys Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu
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tcc gtc atg ggc atc aca ctg gag gag atc gag atc aac gcc gcc ctt  4608
Ser Val Met Gly Ile Thr Leu Glu Glu Ile Glu Ile Asn Ala Ala Leu
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ccc atc aac ccc aac atc atc cgt atc atg cgt gtt ctg cgt atc gcc  4656
Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala
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Arg Val Leu Lys Leu Leu Lys Met Ala Thr Gly Met Arg Ala Leu Leu
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gac aca gtg gta cag gct ctg tcc cag gtg ggc aac ctg ggc ctg ctc  4752
Asp Thr Val Val Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu
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Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe
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gga aag ctg gtc tgc aat gac gag aac ccg tgt gag ggc atg agc cgc  4848
Gly Lys Leu Val Cys Asn Asp Glu Asn Pro Cys Glu Gly Met Ser Arg
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cac gcc acc ttt gaa aac ttc ggc atg gcc ttc ctc acg ctc ttc cag  4896
His Ala Thr Phe Glu Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Gln
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gtc tcc acg ggc gat aac tgg aat gga att atg aag gac acc ctg cga  4944
Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg
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gac tgt acc aat cat gag cgc acg tgc cta agc agc ctg cag ttt gtg  4992
Asp Cys Thr His Asp Glu Arg Thr Cys Leu Ser Ser Leu Gln Phe Val
    1650                1655                1660

tca ccg ctc tac ttt gtg agc ttc gtg ctc acg gct cag ttc gtg ctc  5040
Ser Pro Leu Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu
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Ile Asn Val Val Val Ala Val Leu Met Lys His Leu Asp Asp Ser Asn
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Lys Glu Ala Gln Glu Asp Ala Glu Met Asp Ala Glu Ile Glu Leu Glu
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Met Ala His Gly Leu Gly Pro Cys Pro Gly Pro Cys Pro Gly Pro Cys
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gac acc gag agt cac ctg tgc cgg cgc tgc tat tct cta gat gag gag   5328
Asp Thr Glu Ser His Leu Cys Arg Arg Cys Tyr Ser Leu Asp Glu Glu
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acc ctg tgg ctg gac agc gtc tct tta atc ata aag gat tcc ttg gag   5376
Thr Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys Asp Ser Leu Glu
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Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser Val Phe Xaa His
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Tyr Ala Ser Ser Asp Gly Cys Gly Lys Cys His His Asp Lys Gln Glu
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1825                1830                1835
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<400> 13

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  1               5                  10                  15

Lys Met Ala
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INTERNATIONAL SEARCH REPORT

Interna ial Application No
PCT/US 98/23161

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/705 C07K16/28 C12N5/10 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 04144 A (NEUREX CORP) 9 February 1995	1,2,7, 10-18, 20-22
Y	see abstract; claims 1-10	3,19
X	NOONEY JM (REPRINT) ET AL: "Identifying neuronal non-L Ca2+ channels - more than stamp collecting?" TRENDS IN PHARMACOLOGICAL SCIENCES, 10-1997, 18, 363-371, XP002093637 see page 369, right-hand column - page 370, right-hand column	1,2, 10-16, 20-22

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[X] Further documents are listed in the continuation of box C. [X] Patent family members are listed in annex.

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'P' document published prior to the international filing date but later than the priority date claimed

'T' later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

'X' document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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'&' document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
16 February 1999	09/03/1999

Name and mailing address of the ISA	Authorized officer
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INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/US 98/23161

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ERTEL S I ET AL: "Low-voltage-activated T-type Cachannels" TRENDS IN PHARMACOLOGICAL SCIENCES, vol. 18, no. 2, February 1997, page 37-42 XP004055849 see page 39, left-hand column, paragraph 4 - page 40, middle column, paragraph 1; table 1	1,2, 10-16, 20-22
X	DZHURA IO ET AL: "Characterization of hypothalamic low-voltage-activated Ca channels based on their functional expression in Xenopus oocytes." NEUROSCIENCE, FEB 1996, 70 (3) P729-38, XP002093638 UNITED STATES see the whole document	1,2, 10-18, 20-22
Y	WILSON R ET AL: "2.2 MB OF CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III OF C ELEGANS" NATURE, vol. 368, 3 March 1994, pages 32-38, XP002910426 see abstract	3,19
Y	& EMBL DATABASE Accession number q18840 WILSON R. ET AL. 1996 see the whole document	3,19
A	WO 93 04083 A (SALK INST BIOTECH IND) 4 March 1993 see abstract; claims 1-39	1-22
P,X	PEREZ-REYES E ET AL: "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel 'see comments!'" NATURE, FEB 26 1998, 391 (6670) P896-900, XP002093639 ENGLAND see the whole document	1-15, 20-22
P,X	CRIBBS LL ET AL: "Cloning and characterization of alphaIH from human heart, a member of the T-type Ca2+ channel gene family." CIRC RES, JUL 13 1998, 83 (1) P103-9, XP002093640 UNITED STATES see the whole document	1-22

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INTERNATIONAL SEARCH REPORT

Information on patent family members

Inter ional Application No
PCT/US 98/23161

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